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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2 (bases 1 to 2339)
Hu,H.M., O'Rourke,K., Boguski,M.S. and Dixit,V.M.
Direct Submission
Submitted (07-CCT-1994) Department of Pathology,
Nichigan Medical School, 1301 Catherine St., Ann
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2339)
Hu,H.M., O'Rourke,K., Boguski,M.S. and Dixit,V.M.
A novel RING finger protein interacts with the cytop of CD40
J. Biol. Chem. 269, 30069-30072 (1994)
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The Epstein-Barr virus transforming proteins for the tumor necrosis fact Cell 80 (3), 389-399 (1995) 95163092
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Genetics, Harvard Medical School, 75 Francis Street, Boston,
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Matches 2276; Conserv 541 481 301 601 541 601 481 421 361 421 241 301 241 181 122 838 721 778 661 718 658 361 181 121 61 62  $\vdash$ aaaatgaggcccaaagaagtgatgccacttggttaaggtcccagagcaggtcagaatcag cgcttctgcgagagctgcatggcggccctgctgagctcttcaagtccaaaatgtacagcg tacaagtgtgagaagtgccacctggtgctgtgcagcccgaagcagaccgagtgtgggcac cctgacagaagaactcctctttcctaaaatggagtcgagtaaaaagatggactctcct ggcgcgctgcagactaacccgccgctaaagctgcacactgaccgcagtgctgggacgcca acctaggatcagaaacctggctcctggctcct-gctccctactcttctaaggatcgctgt 180 cagactctcctgaggagcgagttgagtgcacacttgtcagagtgtgtcaatgcccccagc aaacacgaagacaccgactgtccctgcgtggtggtgtcctgccctcacaagtgcagcgtc aaataccgggaagccacatgcagccactgcaagagtcaggttccgatgatcgcgctgcag TGTCAAGAGAGCATCGTTAAAGATAAGGTGTTTAAGGATAATTGCTGCAAGAGAGAAATT CCTGACAGAAGAGAACTCCTCTTTCCTAAAAATGGAGTCGAGTAAAAAGATGGACTCTCCT **ACCTAGGATCAGAAACCTGGCTCCTGGCTCCTGGCTCCTACTCTTAAGGATCGCTGT** AAACACGAAGACACCGACTGTCCCTGCGTGGTGGTCCTGCCCTCACAAGTGCAGCGTC 899 Conservative ĝ KTVEDKYKCEKCHLVICSPKQTECGHRECESCMAALLSSSSRCTAGQESIVEDKVFK
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DP\* 1858. .2359 1 533 c 95.7%; 0; Score 2238.8; Pred. No. 0; 0; Mismatches g 멂 2; 10; Indels Length 2359; 6 Gaps 240 360 60 121 777 660 717 600 657 540 600 480 540 420 480 360 420 300 240 120 897 Ψ

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Submitted (15-FEB-1995) Seth
University, 630 W. 168th St.,
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Verentheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2455)
Cheng,G., Cleary,A.M., Ye,Z.S., Hong,D.I.,
Baltimore,D.
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Science 267 (5203), 14
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                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 (bases 1 to 2240)
Sato, T., Irie, S. and Reed, J.C.
A novel member of the TRAF family of putative signal proteins binds to the cytosolic domain of CD40 FEBS Lett. 358 (2), 113-118 (1995)
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DINCOLKREILALQIYCRNESGCAPKCSVQTLLRSEG
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/gene="CAP-1"
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/db_xref="taxon:9606"
/dev_stage="fetus"
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Db 1126 Qy 1332 Qy 1392 Qy 1392 Qy 1452 Qy 1512 Qy 1512 Qy 1572 Qy 1572 Qy 1572 Qy 1572 Qy 1632 Qy 1632 Qy 1752 Qy 1812 Qy 1812 Qy 1812 Qy 1932 Qy 2052 Qy 2172 Qy 2232	Db 1006  Qy 1212  Db 1066
CTCCCTCCCADAACCGCGTGACCAGCTGGACCAGACCAGGACCAGGACCAGGACCAGGGCCAACTGGC   CTGGGAACCACCGCGTGACCAGCTGGACCTGACCGGGACCAGGGCCCCGGGCCAACTGGC   CTGGCAACCACCGCCTTGCCCTTCCAGCTCCAGCTCCAGGGCCCAGCCCCCCCC	

Length Indels

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Gaps

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1 (bases 1 to 731)
Wang, X., Bornslaeger, E.A., Haub, O., Tomihara-Newberger, C., Ionberg, N., Dinulos, M.B., Disteche, C.M., Copeland, N., Gilbert Jenkins, N.A. and Lacy, E.
A candidate gene for the amnionless gastrulation stage mouse mutation encodes a TRAF-related protein Dev. Biol. 177 (1), 274-290 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-AUG-1995) Xin Wang, Molecular Biology, Memorial Sloan-Kettering Cancer Center, 1275 York Avenue, New York, NY
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       ACAACCAGATCTGCAGCTTTGAGATCGAGATTGAGAGGCAGAAGGAGATGCTCCGAAACA
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RESULT 7
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HTG R-365N19,

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AUTHORS
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Contig 4: length 23279 bp
Contig 6: length 117351 bp
Contig 5: length 27145 bp.
Contig 5: length 27145 bp.
* NOTE: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence ontigs
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - Web: www.genoscope.cns.fr)
On Feb 16, 2000 this sequence version replaced g1:6065792.
IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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98; Conservative
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1 18959: contig of 18959 bp in length
18960 19959: gap of 1000 bp
137310: contig of 177351 bp in length
137311 138310: gap of 1000 bp
138311 161000: contig of 22690 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given, however the sizes of the gaps between them are based on estimates that
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mmalia; Eutheria; Primates;
(bases 1 to 161000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone=11b="RPC1-11"
/clone="R-965N19"
30007 .30150
                                                                                                                                                                                                         /note="matching EMBL:R51760;
software (G. Schuler)"
a 37469 c 38715 g 43572 t
                                                                                                                                                                                                                                                                                         /standard_name-"L38509"
/note-"matching EMBL:L38509;
software (G. Schuler)"
129669. .129777
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software (G. Schuler)"
124129. 124260
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/note="matching EMBL:z233999; Identified using
software_(G__Schuler)"
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                                                                                                   42.6%;
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                                                                                  Score 996.8;
Pred. No. 4.1e
0; Mismatches
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                                                                                  4.1e-210;
ches 2;
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ACCESSION VERSION

partial c Homo sapiens

cds;

TNF-receptor and 3'UTR. 5844 bp

associated factor-3

(TRAF-3) mRNA,

AF110908.1

GI:4761209

DEFINITION

AF110908

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RESULT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5844)

van Eyndhoven, W.G., Frank, D., Kalachikov, S., Cleary, A.M.,
Hong, D. I., Cho, E., Nasr, S., Perez, A.J., Mackus, W.J.M., Cayanis, E.,
Wellington, S., Fischer, S.G., Warburton, D. and Lederman, S.
A single gene for human TRAF-3 at chromosome 14d32.3 encodes a
variety of mRNA species by alternative polyadenylation, mRNA
splicing and transcription initiation
Mcl. Immunol. 35 (18), 1189-1206 (1998)
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van Eyndhoven, W.G., Frank, D., Kalachikov, S., Cleary, A.M., Hong, D.I., Cho, E., Nasr, S., Perez, A.J., Mackus, W.J.M., Cayanis, E., Wellington, S., Fischer, S.G., Warburton, D. and Lederman, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-DEC-1998) Medicine, Columbia University, 630 West
168th Street, New York, NY 10032, USA
Location/Qualifiers
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/product="TNF-seceptor associated factor-3"
/protein_id="AAD29276.1"
/db_xref="GI:4761210"
/translation="VFVAQTVLENGTYIKDDTIFIKVIVDTSDLPDP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/chromosome-"14"
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Pred. No. 6.8e-106;
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primer_bind
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KEYWORDS
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AUTHORS
TITLE
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Query Match
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Matches 425; Conserv
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STS sequence; primer; sequence tagged site.
human vector=pJCP1 host=E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XX individual of French nationality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STS size: 230
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Pediatrics, Tel: (319) 356-3508 Fax: (319) 356-3347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synonyms: UTR_05642_U15637, CHLC.UTR_05642_U15637.T36426
Contact: Dr. Jeffrey C. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cooperative Human Linkage Center Unpublished (1995)
                                                                                                                                                                                                                                                                           Buffer: :
                                                                                                                                                                                                                                                                                                                                                                           Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer A: AGAGCACACCTGACACGTTT Primer B: CTGACATGTCCAGCTATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: jeff-murray@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 425)
Murray, J., Sheffield, V, Weber, J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata; Tetrapoda; Amnlota; Mammalla; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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human STS CHLC.UTR_05642_U15637.P65624 clone UTR_05642_U15637
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1. .425
                                                                                                               /organism="Homo sapiens"
154. .391
154. .173
                                                                                  complement(372..391)
4 81 c 101 g
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KCl: 50mM
Tris: 10mM
pH: 8.3
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extension:
PCR cycles:
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Primer:
            18.2%; Score 425; DB 13; 100.0%; Pred. No. 1e-83;
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Mus musculus mRNA for
D83528 D83528.1 GI:1549145
TRAF5.
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Submitted (15-FEB-1996) to the DDBJ/EMBL/GenBank databases.
Jun-ichiro Inoue, Institute of Medical Science, University of Tokyo, Oncology; 4-6-1 Shirokanedal, Minato-Ku, Tokyo 108, Japan Tokyo, Oncology; 4-6-1 Shirokanedal, Tokyo 108, Japan
                                                                                                                                                         Ishida,T.K., Tojo,T., Aoki,T., Kobayashi,N., Ohishi,T., Watanabe,T., Yamamoto,T. and Inoue,J. TrAF5, a novel tumor necrosis factor receptor associated family protein, mediates CD40 signaling Proc. Natl. Acad. Sci. U.S.A. 93 (18), 9437-9442 (1996)
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus cDNA to Mus musculus
                                                                                                                                                                                                                                       Unpublished (1996)
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Location/Qualifiers
                                                                 /organ1sm="Mus musculus"
/db_xref="taxon:10090"
188. .1864
/product="TRAF5"
/protein_id="BA11942.1"
/db_xref="Gi:1549146"
/translation="MAHSEEQAAVPCAFIRQNSGNSISLDFEPDTEYQFVEQLEERYK
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VLNLHYYCKNAPGCNARIILGRFQDHLQHCSFQAVPCPNESCREAMLRKDVKEHLSAY
CRFREEKCLYCKRDIVVTNLQHBENNSCPAYPYSCPNRCQTIPRARVNEHLIVCPEA
EQDCPFKHYGCTYKRGKRGNLLBHERAALQDHMLLVLEKNYQLEQRISDLYQSLEQKES
KLQQLAETYKKFFKELKGFTQMFGRNGTFLSNVQALTSHTDKSAWLEAQVRQLLQIVN
QQPSRLDLRSLYDAVDSVKQRITQLEASDQRLVLLEGETSKHDAHINIHKAQLNKNEE
RFKQLEGACYSGKLIWKYTDYRVKKREAVEGHFYSVFSQPFYTSRCGYTLCARAYLNG
DGSGKGTHLSLYFVMRGEEDSLLQWPFRQRVTLMLLDQSGKKNHIVETFKADPNSSS
FKKRDDGENNIASGCPRFYSHSTLENSKNYYIKDDTLFLKVAVDLTDLEDL"
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Pred. No. 6.9e-69;
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Direct Submission
Submitted (23-0CT-1995) to the DDBJ/EMBL/GenBank databases
Hiroyasu Nakano, Juntendo University School of Medicine, De
of Immunology; 2-1-1 Hongo, Bunkyo-ku, Tokyo 113, Japan
(E-mail:hnakano@med.juntendo.ac.jp, Tel:03-5802-1045,
Fax:03-3813-0421)
                                                                                                                                                                                                                                                                        MUSCRDA 2222 bp
Mouse mRNA for TRAF5
D78141
                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 2222)
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GAAAGACGTGAAAGAGCACCTGAGCGCATACTGCCGGTTCCGAGAGGAGAAGTGCCTTTA
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Biol. Chem. 271 (25), 14661-14664 (1996)
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cafchsylhnphqtgcghrfcqqcirslrelnsvpicpvdkyikpqbvykbnckke
vlulhyycknapgcnatiilgreqdhlqhcsfqavpccpescreamlrkdvkehlspy
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crfreekcliyckrdivythqdheenscpayfvgcpvrcvqtiprarvnehltycpax
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kiqqlaetvkkfekelkqftqmfgrngtflsnvqaltshtdxsamleaqvrhllqivn
qppsrldlrslydavdsykgrtqleasdqrlyllegstskhapatgrhukkne
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DGSGKGTHLSLYFVVMRGEFDSLLQWPFRQRVTLMLLDQSGKKNHIVETFKADPNSSS
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/protein_id="BAA11218.1"
/db_xref="GI:1469893"
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/db_xref="taxon:10090"
/cell_line="J774A.1"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2738)
Nakano,H., Shindo,M., Yamada,K., Yoshida,M.C., Santee, Ware,C.F., Jenkins,N.A., Gilbert,D.J., Yagita,H., Cope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TNF receptor-associated face expression and assignment of the Genomics 42 (1), 26-32 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-SEP-1996) Department of Immunology, University School of Medicine, 2-1-1 Hongo, Bunkyo
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DYKMKKREAVDGHTVSIFSQSFYTSRCGYRLCARAYLNGDGSGRGSHLSLYFVVMRGE
FDSLLQWPFRQRVTLMLLDQSGKKNIMETFKPDPNSSSFKRPDGEMNIASGCPRFVAH
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/note="TRAF5"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JAN-1997) to the DDBJ/EMBL/GenBank databases. Seiichi Mizushima, Mochida Pharmaceutical Co.,LTD, Biosciences Research Laboratory, 1-1, Kaniya 1-chome, Kita-ku, Tokyo 115, Japan (E-mail:smizushi@mochida.co.jp, Tel:03-3913-6261)
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KIQQLABTIKKLEKEFKQFAQLFGKNGSFLPNIQVFASHIDKSACHARAVLAQLSKNEE
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RFKLEGTCYNGKLIWFAVDTVKQKITLLENNDQRLAVLEEENKHDTHINIHKAQLSKNEE
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KRPDGEMNIASGCPRFVAHSVLENAKNAYIKDDTLFLKVAVDLTDLEDL
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/db_xref="GI:2982671"
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JOURNAL REFERENCE AUTHORS RESULT 14 AC016192 LOCUS REFERENCE AUTHORS TITLE SOURCE ORGANISM DEFINITION KEYWORDS ACCESSION VERSION E 2 (bases 1 to 157851)

B Sirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

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Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Mammalia; Butheria; Primates; Can 1 (bases 1 to 157851) Birren, B., Linton,L., Nusbaum,C. Homo sapiens, clone RP11-24B10 AC016192 AC016192.4 GI:7407937 HTG; HTGS\_PHASE1; HTGS\_DRAFT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. pieces AC016192 Unpublished sapiens clone sapiens 157851 bp DNA RP11-24B10, WORKING and Lander, E DRAFT SEQUENCE, 13 unordered 04-APR-2000

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the configs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 150583 bases at least Q40 Consensus quality: 153610 bases at least Q30 Consensus quality: 155123 bases at least Q20
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t, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                       115647 115746: gap of 100 bp 115747 157851: contig of 42105
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1243 1342: gap of 100 bp
1343 2590: contig of 1248 bp in length
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25 6824: gap of 100 hm
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                                                                                                                                                             /clone="RP11-24B10"
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100 bp

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8845: gap of 1921 bp in length

14718: contig of 5873 bp '-

14818: gap of

19129: contig of 5873 bp '-
                                            note="assembly_fragment"
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e="assembly_fragment"
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* NOTE: This record contains 94 individual

* sequencing reads that have not been assembled into

* sequencing reads that have not been assembled into

contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49960)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.H.
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Search completed: September Job time: 6953 sec 'n 2000, 09:55:55

THIS PACE BLANK (USPTO)

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Title:
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Maximum Match 100%
Listing first 45 summaries
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9324.596 Million cell updates/sec
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gb\_est40: gb\_est41: gb\_est42:

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gb\_est48:\* gb\_est49:\* gb\_est50:\* gb\_est51:\* em\_est35:\* em\_est36:\*

em\_est37

em\_gss2:\* em\_gss3:\*

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Result

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Score

Query Match

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SUMMARIES

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
AA811607 693 bp mRNA EST 19-FEB-1998 ob74a11.52 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337084 3's similar to TR:Q12990 Q12990 CD40 BINDING PROTEIN. [2] TR:Q13076;
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AL582315 tq66d06 x
AW081351 xc41b10 x
AA625253 aL68b04 r
AA6232920 zr48b02.r
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AI549245 UI-R-C3-t
AA086724 mn92f10.r
AI844378 UI-M-AL1-
AI870206 w120a06.x
AI241380 qth74a09.x
AA847855 ocd39b01.s
AW297776 UI-H-BW0-
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AA655885 vs42h01.r
AA655885 vs42h01.r
AI180123 EST223860
AI322855 ms69b11.y
AW421297 f189f01.y
AM421297 f189f01.x
AM631851 91400 MAR
AM631851 91400 MAR
AM631851 91400 MAR
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AA200146 mu06h08.r
N59366 yz87d10.s1
AA233337 zr48b02.s
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AQ879659 HS_4821_A
AQ879711 HS_4821_A
AI432683 th45a02.x
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W40768 mc38d11.rl
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AI393367 tg44e06
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AL061969 Drosophil
W136067 UI-H-BI1-
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ms69bll.x
63060 MAR
102410 MA
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                                                                                             ATCGTTAAAGATAAGGTGTTTAAGCATAATTGCTGCAAGAGAGAAATTCTGGCTCTTCAG
                                                                                                                                                                                                                                                                                                                     652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
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Contact: Robert St
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AA811607.1 GI:2881218
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1169 Std Error: 0.00
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1 (bases 1 to 693)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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nilarity 94.1%;
Conservative
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/clone_lib="NCI_CGAP_GCB1"
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CNS005YQ AW136067 AA462939

ALIGNMENTS

AA200146 N59366 AW484898 AW653633

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AA186061 AI549479 AW420948

114.6 111.4 105.6 104.4 98.4

AW631851 AA165848 AW089918 AQ879659 AQ879711 AI432683 AW631537 AI528865

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196.2 194 192.8 191.6 175.4

417 424 491 491 491 481 603 380 380 3180 462

A1870206 AA1241380 AA2847855 AW297716 AA619651 AA655885 AA1180123 AA1322855

AA086724 AI844378

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377.4 359.6 344.8 332.8 305.8 213.6 213.6

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Insert Length: 651 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 448.
                                                                                                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D.,
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National Cancer Institute, Cancer Genome Anatomy
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NCI_CGAP_Co16 Homo
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                                                                                                                                     AL135246 587 bp mRNA

DKF2D762M1613_r1 762 (synonym: hmel2)

DKF2D762M1613 5', mRNA sequence.

AL135246.1 GI:6603433
Eukaryoia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 587) Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subtraction by Bento Soares and M. Fatima Bonaldo. 132 \, \mathrm{c} 111 \, \mathrm{g} 181 \, \mathrm{t}
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Pred. No. 4.8e-139;
0; Mismatches 1;
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              GAATTATTTATCCTTCAACAAGATAAATATTGCTGTCAGAGAAGGTTTTCATTTTCATTT
                                                                                                                             gaattatttatccttcaacaagataaatattgctgtcagagaaggttttcattttcattt 2177
                                                                                                                                                                        GAGCCACGCGTGAGCACACCTGACACGTTTTATAATAGACTAGCCACACTTCACTCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No sl sequence available.
This clone (DKFZp762MG13) is available at t
Please contact the RZPD: Ressourcenzentrum,
Berlin-Charlottenburg, GERMANY; Email: clone
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone from S. Wiemann, Molecular Genome Analysis, German Can-
Research Center (DKF2); Email s.wiemann@tkf2- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of
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This is the
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On Apr 7, 1998 this
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/db_xref="taxon:9606"
/clone="DKF2p762M1613"
/clone_11b="762 (synonym: hme12)"
/tissue_type="meianoma (MeWo cell 1:
/dev_stage="adult"
/lab_host="DH10B"
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99.2%;
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Pred. No. 1.5e-137;
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Matches 554
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acttcggatctgcccgatccctgataagtagctggggaggtggatttagcagaaggcaac 1950
                                                                                  gttctagaaaatgggacatatattaaagatgatacaatttttattaaagtcatagtggat 1890
                                                             GTCCTAGAAAATGGGACATATTAAAGATGAT-CCATTTTTATTAAAGTCATAGTGGAT
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similar to
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Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
On Oct 30, 1998 this sequence version replaced
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer:
High qualit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.iln1.gov/bbrp/image/image.html
Insert Langth: 719 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                       pooled lung tumor tissue, and was then primed with a Not oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                        Fatima Bonaldo. "
147 c 131
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/note-"Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:2213771"
/clone_lib="NCI_CGAP_Lu19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
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Primates;
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Pred. No. 4.1e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW081351 563 bp mRNA EST 14-OCT-1999 xc41b10.x1 NCI_CGAP_CO20 Homo sapiens cDNA clone IMAGE:2586811 similar to TR:Q13947 Q13947 CD40-ASSOCIATED PROTEIN. ; contains LTR1.t2 LTR1 repetitive element ;, mRNA sequence.
AW081351
                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                          Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                             High
                                                                                                                                                                                                                                                                         Tissue Procurement: Christopher A. Moskaluk, M.D., ph.D., Michi
R. Emmert-Buck, M.D., Ph.D. Compart Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, Th
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                            Possible reversed clone: polyT not found
                                                                                                                                                             primer: -40UP from Gibco
                                                                                                                            quality sequence stop: 427.
Location/Qualifiers
             /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2586811"
/clone_lib="NCI_CGAP_CO20"
/tissue_type="moderately differentiated
/lab_host-"DH10B"
 colon; Vector:
pcmv-sport6;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E

Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

E 1 (bases 1 to 529)

S Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Mar

Marrin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan

Theising,B., White,Y., Wylie,T., Waterston,R. and Wil

Washin-NCI human EST Project

L Unpublished (1997)

On Jan 17, 1998 this sequence version replaced gi:190

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 631
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a 149 c 132 g 157 t
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Soares_NhHMPu_S1 Homo
to TR:G695358 G695358
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2.2e-120;
7;
                                                                                                                                           Dubuque, T., Geisel, G., Jost, S
                                                                                                                                                                                                                                                                                                  EST 15-OCT-1997 sapiens cDNA clone IMAGE:1047151 CD40-ASSOCIATED PROTEIN: ;, mRNA
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Wilson, R.
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                                                                                                         gaaaaggtcttgaggaaagacctgcgagaccacgtggagaaggcgtgtaaataccggggaa
                                                                                                                                                                 GTGCATGTAGAAAATGAGTGCCATGTTGAAGAAGTTGCATGTGTGCGTCCTGACTGCAAA 110
                                                                                                                                                                                     gtgcatttaaaaaatgattgccattttgaagaacttccatgtgtgcgtcctgactgcaaa
                                                                                                                                                                                                                                              ATCTATTGTCGGAATGAAAGCAGAGGTTGTGCAGAGCAGTTAACGCTGGGACATCTGCTG
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            GCCACATTCAGGCGCTGCAAGAGTCAGGTTGCGATGATCGCGCTGCAGA
                                                                                    GAAAAGGTCTTGAGGAAAGACCTGCGAGACCACGTGGAGAAGGCGTGTGAATACCGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-*organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NDHPU, and fetal heart NDHHJ9W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 48488-89479.
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/clone="IMAGE:1047151"
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Pred. No. 3.1e-112;
0; Mismatches 30;
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Best Local
                                                                                                                                                                                                                                                           Matches 486;
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gggcaccgcttctgcgagagctgcatggcggccctgctgagctcttcaagtccaaaatgt 474
                                                                              ACGCCAGTTTTTGTCCCTGAACAAGGAGGTTACAAGGAAAAGTTTGTGAAGACCGTGGAG 432
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zr48b02.rl
similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 486.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Wohldmann,P. and
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project Unpublished (1995)
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Fax: 314 286 1810
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                           106
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                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHU), and fetal heart NbHH19W) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 360232-265223, 340488-34549, and 484488-489479."
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/db_xref="GDB:5560570"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:666603"
/clone_lib="Soares_NhHMPu_S1"
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Pred. No. 3.1e-108;
D; Mismatches 2;
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zr37d03.rl
similar to
                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is avallable royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
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                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
Contact: Wilson RK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
1 (bases 1 to 658)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M
Holman,M., Hultman,M., Kucaba,T., Lew,M., Lennon,G., Marr
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P.
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Location/Qualifiers
/note-"Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA
                                                                                          pregnant uterus"
/lab_host="DH10B"
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/clone="IMAGE:665573"
/clone_lib="Soares_NhHMPu_S1"
/tlssue_type="Pooled human mei
                                                                                                                                                                                        organism-"Homo sapiens"
/db_xref-"GDB:5427605"
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ares. NhHMPu.S1 Homo sapiens cDNA
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n,G., Marra,
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gccactgcaugagtcaggttccgatgatcgcgctgcagaaaca 782
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                                                                                                                                                                                                                                                                                                               GCCACTGCAAGAGTCAGGTTCCGATGANTCCGCTGCAGAAACA
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Eukaryota; Metazoa; (
Mammalia; Eutheria; 1
1 (bases 1 to 404)
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                                                                                                                                                sequence.
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                                                                                                                                                                                404 bp mRNA
NCI_CGAP_GC6 HOMO
TR:Q13947 Q13947 C
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                                                                                                                                                                                A EST 22-MAR-2000 o sapiens cDNA clone IMAGE:2946911 CD40-ASSOCIATED PROTEIN. ;, mRNA
                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
.5e-107;
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                                    Hominidae;
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Anatomy Project (CGAP),

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                                                                                                                                                             atgggacatatattaaagatgatacaatttttattaaagtcata 1884
                                                                                                                                                                                                                                                                       ctggagagatgaatatogoctctggctgcccagtctttgtggcccaaactgttctagaaa 1840
                                                                                                                                                                                                                                                                                                                                                         GACGTCATTTGGGAGATGCATTCAAGCCCGACCCCAACAGCAGCAGCTTCAAGAAGCCCA
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                                                                                                                                                                                                                                              CTGGAGAGATGAATATCGCCTCTGGCTGCCCAGTCTTTGTGGCCCAAACTGTTCTAGAAA
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -400P from Gibbo.
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Contact: Robert Strausberg, Ph.D
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/db_xref="taxon:9606"
/clone="IMAGE:2946911"
/clone_lib="NCI_CGAP_GC6"
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       gcccaaagaagtgatgccacttggttaaggtcccagagcaggtcagaatcagacctagga 129
  ccctgaacaaggaggttacaaggaaaagtttgtgaagaccgtggaggacaagtacaagtg
                                                                                    GCAGACTAACCCGCCGCTAAAGCTGCACACTGACCGCAGTGCTGGGACGCCAGTTTTTGT
                                                                                                                gcagactaaccogcogctaaagctgcacactgaccgcagtgctgggacgccagtttttgt 308
                                                                                                                                                                                           AAGAGAACTCCTCTTTCCTAAAATGGAGTCGAGTAAAAAGATGGACTCTCCTGGCGCGCT
                                                                                                                                                                                                                                                                                                                               tcagaaacctggctcctggctcct-gctccctactcttctaaggatcgctgtcctgacag 188
                                                                                                                                                                                                                                                                                                                                                                                                              GCCCAAAGAAGTGATGCCACTTGGTTAAGGTCCCAGAGCAGGTCAGAATCAGACCTAGGA 194
                                                                                                                                                                                                                                                                                                      TCAGAAACCTGGCTCCTGGCTCCCTACTCTTCTAAGGATCGCTGTCCTGACAG
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Contact: Robert Stratel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gow) for further information. Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found Strand Possible reversed clone: polyT not found Strand Possible reversed clone: polyT not found Standard Possible reversed polyT not found 
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Mammalia; Eutheria;
1 (bases 1 to 510)
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2603170"
/clone_lib="Soares_NFL_T_GBC_S1"
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/db_xref="taxon:9606"
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97.5%;
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Primates;
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Best Local Similarity
Matches 382; Conserv
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                                       ACGCGCCCGGCCCCTGAGCCGGCCGAGCGGCGACGGACCGCGAGATGAGGAAAATGAG 134
                                                                                                                                             acgcgcccggcgcccctgagccggccgagcggccgacggaccgcgagatgaggaaaatgag 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctgcgagagctgcatg 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INGAGAGTGCCACCTTGGTGCTGCAGCCCGAAGCACCCGAGTGTGGGCCACCCGCTT 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgagaagtgccacc-tggtgctgtgcagcccgaagcaga-ccgagtgtgggca-ccgctt 425
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tcagaaacctggctcctggctcct-gctccctactcttctaaggatcgctgtcctgacag 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 477)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI393367 477 bp mRNA EST 30-MAR-1999 tg44e06.x1 Soares.NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111650 3' similar to TR:Q13947 Q13947 CD40-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN. ;, mRNA sequence. AI393367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Seq primer: -40UP from Gibco
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Location/Qualifiers
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2111650"
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/lab_host="DH10B"
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                                                                                                                                                                                                       Score 359.6; DB 39;
Pred. No. 2.2e-84;
0; Mismatches 19;
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N76469/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcagactaaccogcogctaaagctgcacactgaccgcagtgctgggacgccagtttttgt 308
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YZ87d10.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens CDNA
Clone IMAGE:290035 5' similar to PIR:A55649 A55649 TNFR-associated
Protein LAP1 - human ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
On Jan 6, 2000 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier;L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   שיייים γοτα; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (dases 1 to 475)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: reverse ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 291.
Location/Qualifiers
                  double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified PT713 vector (Pharmacia). Library went through one round of
                                                                                                          /tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="TDH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st_strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:3905875"
/db_xref="taxon:9606"
/clone="IMAGE:290035"
                                                                                                                                                                                                                                                                                         /clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                               1. .475
normalization to a Cot = 5. Library constructed by Bentc
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TITLE
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                                            on Jan 7, 1998 this sequence version repla
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                    W40768 535 bp mRNA EST 11-SEP-1 mc38d11.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:350805 5' similar to gb:U21050 Mus musculus CD40 recassociated factor 1 (MOUSE); mRNA sequence.
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1 (bases 1 to 535)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                   The WashU-HHMI Mouse EST Project
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mouseest@watson.wustl.edu
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sequence.
AA504259
AA504259.1
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Seq primer:
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aa61b08.51 NCI_CGAP_GG
similar to TR:G695358
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)
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/lab_host="Tillin resist
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CB1 Homo sapiens cDNA clone IMAGE:825399
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                                                   agtaaaaagatggactctcctggcgcgctgcagactaacccgccgctaaagctgcacact 279
                                                                                                                                                                     CCCAGAGCAGGTCAGAATCAGACCTAGGATCAGAAACCTGGCTCCTGGCTCCTGGCTCCC 192
                                                                                                                                                                                                 cccagagcaggtcagaatcagacctaggatcagaaacctggctcctggctcct-gctccc 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Louis M. Staudt, M.D., Ph.D., Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Oct 31, 1997 this sequence version replaced gi:1520960 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Cancer Institute, Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:825399"
/clone_lib="NCI_CGAP_GCB1"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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r Institute, Cancer Genome Anatomy Project (CGAP),
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Primates;
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Pred. No. 3.6e-70;
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Fax: 319 335 9255
Email: msoarcs@blue.weeg.uiowa.edu
Oligo-dT:track not found, Not I site shown in beginning of sequence is likely internal to the message.cDNA Library Preparation: M.B. Soarcs Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LINL (info@image.llnl.gov).
IMAGE ID=1785915 The following repetitive elements were found in this cDNA sequence: 164-216, >(GGA)n#Simple_repeat
Seq primer: M13 Forward
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/clone_lib="UI-R-C3"
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                              chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)"

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Search completed: September 2, 2000, 09:01:32 Job time: 7559 sec

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Run on: OM nucleic - nucleic search, using sw model September 2, 2000, 08:09:01; Search time 97.71 Seconds (without alignments) 5989.144 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title:
Perfect score:
Sequence: US-09-224-556-1 2339

1 acgaaggccacgccccggc.....ggagaatttatgaaatagta 2339

Scoring table: IDENTITY\_NUC
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rched: 311585 seqs, 125096042 residues

al number of hits satisfying chosen parameters:

623170

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : N\_Geneseq\_36:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Human GDF-1 cDNA.	Human GDF-1 (fx) p	Human GDF-1 cDNA.	cDNA sequence enco	Human GDF-1(fx) mo	Human GDF-1(fx) mo	Human GDF-1(fx) mo	Human morphogenic	Morphogen GDF-1 co	Human GDF-1 coding	Chimeric endogluca	Continuation (8 of	•

## ALIGNMENTS

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121 gacctaggatcagaaacctggctcctggctcctgctcctactcttctaaggatcgctgt 180	ACGAAGGCCACAGCCCCCGGCGCCCCTGAGCCGAGCGGCGACGGACCGCGAGATGAG  gaaaatgaggccaaaggaagtgatgccacttggttaaggtcccagagcaggtcagaatca [	Query Match 99.9%; Score 2337.4; DB 1; Length 2339; Best Local Similarity 100.0%; Pred. No. 0; Matches 2338; Conservative 0; Mismatches 1; Indels 0; Gaps	135251 standard; 135251; 13525

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                     gagcttgacaaggagatccggcccttccggcagaactgggaggaagcagacagcatgaag
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RESULT 2
T90123
ID T90123 standard; cDNA; 2918 BP.
AC T90123;
DT 27-MAR-1998 (first entry)
DE Human CRAF1 (TRAF-3) cDNA.

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pneumoconiosis; adult respiratory distress syndrome; pneumonitis; asbestosis; siliconosis; Farmer's lung; hepatitis; cirrhosis; atherosclerosis; multiple sclerosis; glomerulonephritis; endocarditis; leprosy; malaria; Goodpasture's disease; nephropathy; endocarditis; leprosy; malaria; Goodpasture's disease; Henoch-Schoenlein purpura; polyarteritis; multiple myeloma; Wegener's granulomatosis; cryoimmunoglobulinaemia; waldenstroem's macroglobulinaemia; mayloidosis; Sjogren's sydrome; alds; oesophageal dysmotility; inflammatory bowel disease; bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
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myasthenia gravis; idiopathic thrombocytopaenia purpura;
Graves' disease; haemolytic anaemia; diabetes mellitus; psoriasis;
hyper immunoglobulin E syndrome; apoptosis; infectious disease;
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/note=_"no exon 3 in p70-1 coding sequence"
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Score 2282.2; Pred. No. 0; 0; Mismatches

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2918; 5 Gaps

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Example 1; Fig 1A-P; 158pp; English.

Example 1; Fig 1A-P; 158pp; English.

CC This 2918 bp cDNA sequence encodes CRAFI (TRAF-3) and its deletion CC and alternative splice isoforms (see W27428-37). It is derived CC from several cDNA species from a Raji B cell library. CRAFI CC acids encoding them, can be used to inhibit CD40 ligand activation of cells that express CD40 on their surface, particularly by CC introducing the nucleic acid molecule into the cells, useful to of cells that express CD40 on their surface particularly by CC treat conditions characterised by an aberrant or unwanted level of CC treat conditions characterised by an aberrant or unwanted level of CC a subject receiving transplant organs, or a CD40 dependent inmune crapponse in a subject receiving gene therapy. The condition may be can allergic response, an autoimmune response, or may be dependent on CD40 ligand-induced activation of epithelial cells, an inflammatory kidney disease, a smooth muscle cell-dependent conclicic acids can also be used as probes in diagnostic testing. The gene for CRAFI is located on human chromosome 14932.2.

Sequence 2918 BP; 768 A; 728 C; 822 G; 600 T;
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25-SEP-1997.
21-MAR-1997; U05076.
18-SEP-1996; US-026584.
21-MAR-1996; US-013820.
01-MAY-1996; US-016626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCO ) UNIV COLUMBIA NEW YORK. Cleary AM, Frank DM, Lederman S WPI: 97-479907/44.
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A DNA sequence (T31273) codes for a novel B-cell protein (W03146) termed LMP1 associated protein 1 or LAP1, which strongly associates with the cytoplasmic C-terminal domain (W03148) of Epstein Barr virus (EBV) latent infection membrane protein 1 (LMP1), a domain that is stringently required for transformed cell growth. LAP1 is related to murine tumour necrosis factor receptor associated factor TAFF2. The gene was identified using a yeast 2-hybrid screen. It can be used in gene was identified using a yeast 2-hybrid screen. It can be used in transduction, or for the prodn. of LAP1 polypeptides that inhibit controlling cell growth/tumourigenesis associated with LMP1-encoding viruses, partic. EBV.

Sequence 2359 BP; 668 A; 533 C; 628 G; 530 T;
                                                                                                                                                    Query Match
Best Local Similarity
Matches 2276; Conserv
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28-DEC-1995.
30-DEC-1994: US-367540.
(BGHM ) BRIGHAM & WOMENS H
(REGC ) UNIV CALIFORNIA.
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LMP1 associated protein LAP1 gene.

LAP1; LMP1 associated protein 1; latent infection membrane prot

tumour necrosis factor receptor associated factor; TRAF;

signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AID

Hodgkin's disease; Burkitt's lymphoma; naspharyngeal carcinoma;

mononucleosis; Epstein-Barr virus; EBV; gene therapy; ss.
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mew CD40 associated protein, agonists and antagonists - used to PT modulate cell proliferation, immune response, apoptosis etc., e.g. PT for treating cancer or autoimmune disease PS Claim 13; Fig 1; 94pp; English.

CC This DNA encodes a CD40 associated protein (CAP)-1. The CAP is a protein that specifically binds to CD40, a cell surface receptor involved in capoptosis. Agonists and antagonists of CAP can increase or decrease CC the level of CAP expression in a cell and can thereby modulate the cluction of the cell. Such compounds can be used to treat cancer, autoimmune diseases like asthma, hay fever, rheumatoid arthritis and can tended diseases and neurodegeneration. Antibodies that bind specifically to CAP can be used to assay CAP, to detect pathologically CC altered levels. This nucleic acid can be used to identify related genes and to express CAP for gene therapy.

SQ Sequence 2240 BP; 637 A; 510 C.
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06-JUN-1996.
04-DEC-1995; U15695.
R 02-DEC-1994; US-349357.
7-TOL-) LA JOLLA CANCER R
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23-MAR-1998 (first entry)
CD40 associated protein (CAP)-1 en
CD40 associated protein; CAP; agon
cell proliferation; treatment; can
Homo sapiens.
Key
Location/Qualifies
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137. .1768
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16-OCT-1997.
10-APR-1997.
11-APR-1996: JP-355847.
11-APR-1996: JP-113035.
(MOCH ) MOCHIDA PHARM CO LTD.
Inoue J;
WPI; 97-512716/47.
P-PSDB; W27609.
TRAF5, protein of tumour necrosis farefaily useful in immunisation, to proliferation inhibitor
Claim 12; Pages 41-44; 80pp; Japanes.
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27-APR-1998 (first entry)
Murine TRAF5 cDWA.
Murine mouse; TRAF5; tumour nerceptor associated factor famicell proliferation inhibitor; some sp.
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Sequence 2105 BP; 540 A; 530 C; 578 G; 457 T;
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28-AUG-1997.
24-FEB-1997; J00512.
22-FEB-1996; JP-034674.
22-FEB-1996; JP-034674.
(SUME ) SUMITOMO ELECTRIC INF.
(SUME ) SUM Murine Key CDS Tumour necrosis factor receptor associated: TRAFF - useful to study signal transduction factor receptor family Claim 2; Pages 44-46; 69pp; Japanese. The present sequence encodes a novel protein DNA encoding murine TRAF5, a r TRAF5; tumour necrosis factor TNF signal transducer system; WO9731110-A1. 18-MAR-1998 T87039 σ standard; sp. (first Location/Qualifiers 323. .1999 /\*tag= CDNA entry) to mRNA; Ø ra K, a novel CO. , Yagita receptor; 2254 associated factor family transduction in tumour nec TNF ВP protein, H; receptor factor
; TNF; designated family protein, TRAF5, protein which is

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Sequence 2254 BP; 581 A; 576 C; 625 G; 472 T;
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                                                                        AAAGGAGCTTAAGCAGTTCACACAGATGTTTGGCAGAAATGGAACTTTCCTCCTCAAATGT
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Pred. No. 8.4e-88;
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TRESULT TRESUL P-PSDB; W29258.
Tumour necrosis factor receptor associated :
TRAF5 - useful to study signal transduction (SUME ) SUMITONO ELECTRIC IN Nakano H, Nakata M, Okumura WPI; 97-435162/40.
P-PSDB; W29258. CDS 18-MAR-1998 (first entry)
DNA encoding human TRAF5, a no
TRAF5; tumour necrosis factor
TNF signal transducer system; T87040 standard; T87040; WO9731110-A1. Homo sapiens. J00512. Location/Qualifiers 100. .1773 /\*tag= CDNA ៥ mRNA; IND a novel ~ 60 receptor; Yagita 2846 INE ВP receptor c; TNF; factor family ne in tumour ne factor family protein

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Disclosure; Pages 49-52; 69pp; Japanese.
The present sequence encodes a novel protein, designated TRAF5, which a member of the tumour necrosis factor (TMF) receptor associated factor family. The TRAF5 protein has a coiled-coil domain, a leucine zipper motif and binds to lymphotoxin beta receptor and to CD30, but n to CD40 or TMF receptor 2. TRAF5 and its corresponding DNA are useful the investigation of the signal transducer system of the TMF receptor family and the functions of TRAF proteins. They can also be used as probes for research and diagnostic purposes, and investigation of the specific applications of potential therapeutic agents.

Sequence 2846 BP; 874 A; 538 C; 637 G; 797 T;
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                    ttgagagacaaaaggaaatgcttcgaaataatgaatccaaaaatccttcatttacagcgag
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Pred. No. 8.6e-76;
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Human; TRAF5; thumour necrosis factor;
receptor associated factor family; imm
cell proliferation inhibitor; screenir
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screening; inhibitor;
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W09738099-A1. 16-OCT-1997. 10-APR-1997; J 25-DEC-1996; J 11-APR-1996; J

; J01236. ; JP-355847. ; JP-113035.

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Best Local
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Sequence 3993 BP; 1198 A; 798 C; 865 G; 1132 T;
               1106
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proliferation inhibitor
Claim 13; Pages 52-57; 80pp; Japanese.
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             gtcatagtggatacttcggatctgcccgatcccctgataagt
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                                                                                  caaactgttctagaaaatggga-----catatattaaagatgatacaatttttattaaa
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Key Homo Epstein-Barr induced protein EBI6 gene.
EBI6; Epstein-Barr induced protein 6; LAP1;
EBI6; Epstein-Barr induced protein 6; LAP1;
LMP1 associated protein 1; latent infection membrane protein;
tumour necrosis factor receptor associated factor; TRAF;
signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AID
Hodgkin's disease; Burkitt's lymphoma; naspharyngeal carcinoma; mononucleosis; T31274; 23-OCT-1996 T31274 standard; ø (first entry) Epstein-Barr 76. .1: /\*tag= Location/Qualifiers DNA; 2380 ₽P virus;

EBV;

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28-DEC-1995; U16980.
30-DEC-1994; US-367540.
(BGHM ) BRIGHAM & WOMENS H
(REGC ) UNIV CALIFORNIA.
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A DNA sequence (731274) codes for a novel B-cell protein (W03147) induced by Epstein-Barr virus (EBV) infection, termed Epstein-Barr induced protein 6 or EBI6. The protein appears to be the human homologue of murine tumour necrosis factor receptor (TNFR) associated factor TRAFI. The gene can be used in gene therapy protocols for controlling TRAF-mediated TRMF/TNFR signal transduction, or for the prodn. of EBI6 polypeptides that inhibit transduction for use in treating infection and controlling that interacting infection and controlling that the production are controlling that the production and controlling that the production are controlling that the production and controlling that the production are controlling that the production and controlling that the production are controlling that the production and controlling that the production are controlling that the production and controlling that the production are controlling that the production are controlling that the production are controlling that the production and controlling that the production are controlling that the production and controlling that the production are controlling that the production and controlling that the production are c
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07-DEC-1995.
25-MAY-1995; U
27-MAY-1994; U
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A cDNA clone (T12262) coding for tumour necrosis factor receptor associated factor 2 (TRAF2) (R90578) was isolated using a yeast two-hybrid system to assay for proteins that associate with the intracellular domain (ID) of tumour necrosis factor receptor type 2 (TNF-R2). The cDNA is used for prodn. of recombinant TRAF2, a new factor capable of specific association with TNF-R2 ID and CD40. sequence 2121 BP; 506 A; 560 C; 616 G; 439 T;
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Goeddel DV, Rothe M;
WPI; 96-049310/05.
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28-OCT-1994; US-331394.
22-MAY-1995; US-446915.
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25-MAY-1995; U06639.
27-MAY-1994; US-250858.
28-OCT-1994; US-331394.
22-MAY-1995; US-446915.
(GETH) GENENTECH INC.
Goeddel DV, Rothe M;
WPI; 96-049310/05.
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Example 2: Page 69-71; 116pp; English.

A CDNA clone (T12261) coding for tumour necrosis factor receptor associated factor 1 (TRAF1) (R90577) was isolated from a CDNA library pred. from the murine interleukin-2-dependent cytotoxic T-cell line CT6, using probes based on isolated peptides of TRAF1. The cDNA is used for prodn. of recombinant TRAF1, a new factor capable of specific association with the intracellular domain of the type 2 TNF receptor and CD40.
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Mouse TRAF1; tumour necrosis factor receptor associated factor 1;
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RESULT
T86169
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Prognosione 17 (11-q21.3 or 6 q22-q23, useful in breast cancer prognosis and as leukaemia markers

SClaim 1; File 6; 197pp; English.

CC This sequence encodes human CART1 and is deposited as ATCC 97610. The CART1 polypeptide is localised in the nucleus of breast carcinoma cells cand has 3 structural domains. A Cys-rich region is located at the CRART polypeptide is localised in the nucleus of breast carcinoma cells cand has 3 structural domains. A Cys-rich region is located at the CRART finger domain and is probably involved in protein protein binding. CRASC motifier repeats of an HC3HC3 consensus motif. This domain is constitutes three repeats of an HC3HC3 consensus motif. This domain is constitutes three repeats of an HC3HC3 consensus motif. This domain is constituted the CART motifi. The C-terminal part of the CART1 cc protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be involved in protein corresponds to a TRAF domain known to be invol
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(CNRS) CENT NAT RECH SCI.
(CINRM) INST NAT SANTE & RECH MEDICALE.
(UYPA-) UNIV PASTEUR LOUIS.
Basset P, Byrne J, Rio M, Tomasetto
WPI; 97-154263/14.
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Human; CART1; Lasp-1; N
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31-JUL-1996; U12500.
09-AUG-1995; US-002183.
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Lasp-1; MLN 64; MLN 51;
on; RING finger domain; (
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858. .859
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708. .709
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Query Match Best Local Similarity Best Local Sin Matches 193;

56.8%;

Score 90; Pred. No. Mismatches

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                                                 DNA encoding tumour necrosis factor receptor associated factor 6 - useful for screening compounds, for therapy and diagnosis of immune-regulated diseases, etc.

CLaim 4; Page 11-14; 23pp; English.

This cDNA sequence includes a coding region for a novel human finish cDNA sequence includes a coding region for a novel human finish cDNA sequence includes a sociated factor six (TRAF6) cC polypeptide (see W32113), which transcriptionally activates nuclear factor kappa-B. The 2248 bp sequence was isolated from human spleen and umbilical vein endothelial cell cDNA libraries by hybridisation with TRAF oligonucleotide probes. The isolated nucleic acid is used to produce recombinant TRAF6. The recombinant protein is used in a screening method for detecting agents that modulate binding of TRAF6 to natural intracellular targets, while cells containing the TRAF6 gene are used in a screening method for detecting agents that modulate transcription of TRAF6 inducible genes. Both methods are used to identify compounds potentially useful in the diagnosis and treatment of immune-regulated diseases, e.g. infection, genetic disease and disturbed cell growth/regulation such as neoplasia, inflammation and hypersensitivity. Probes and primers able to hybridise to the cDNA sequence are used to detect TRAF6 mutations, to isolate natural TRAF6-encoding sequences, to detect TRAF6 homologues and analogues, and therapeutically to condulate cellular expression, or intracellular concentration of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor receptor associated factor 6 (TRAF6) Tumour necrosis factor receptor associated factor 6; TRAF6; nuclear factor kappa B; immune-regulated disease; infection; genetic disease; cell growth; cancer; inflammation;
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WPI; 97-535866/49.
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30-OCT-1997.
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19-APR-1996;
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PT New isoforms of Stat6 - having differential effects on the primodulation of Stat6 activity in cells Disclosure; Page 61-66; 88pp; English.

CC Disclosure; Page 61-66; 88pp; English.

CC of transcription). The invention relates to attenuated and dominant configurative isoforms of human Stat6 (signal transducers and activators of transcription). The invention relates to attenuated and dominant configurative isoforms of human Stat6. The detection and quantitation of DNA cor mank encoding Stat6 and/or Stat6b and/or Stat6c can be used to detect differential expression of Stat6 isoforms in numerous diseases, including myeloid cancer, asthma, sarcoma, scleroderma, bone marrow fibrosis, complexity complementary sequences. The genomic or cDNA libraries or to identify complementary sequences. The collection of chromosomal aberrations and translocations involving the stat6 gene. Antibodies against the isoforms can be used to detect the presence of Stat6 and/or Stat6b and/or Stat6c in a sample. Because of the crasscription the isolated and purified forms can be used to study gene regulation and in screening assays for identifying drug candidates which may be used as agonists or antagonists. The two polymeptides may also be used in gene therapy protocols. In particular, Stat6b and/or Stat6c can therapeutically modulate the development and differentiation of B and collinational stat6 with functional responses collinational stat6b when compared Stat6 is an attenuated regulator of gene collination of gene compared Stat6 is an attenuated regulator of gene collination of gene compared Stat6 is an attenuated regulator of gene collination of gene compared Stat6 is an attenuated regulator of gene collination of gen
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Best Local
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27-AUG-1998; U17821.
05-JAN-1998; US-07039
27-AUG-1997; US-0560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES Larochelle WJ, Patel B, Pierce JH; WPI; 99-214517/18.
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Pred. No. 1.4e-06;
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                                               Translation enhancing sequences

Example 1; Pages 88-89; 108pp; English.

The present sequence was used in the preparation of a novel chimaeric gene, comprising: (a) promoter recognised by a DNA-dependent RNA polymerase other than eukaryotic RNA polymerase CI; (b) DNA sequence encoding a chimaeric RNA comprising; and 5' cuntranslated regions (UTR), plus an AU-rich heterologous coding sequence; and optionally (c) terminator recognised by the same polymerase as the promoter. The chimeric RNA is uncapped, translated in plant cell cytoplasm to form a protein and includes two translation-enhancing sequences (TES) derived from the 5' and 3' regions of (sub)genomic RNA of a positive stranded RNA plant cell cytoplasm to form a protein and includes two translation gene can be used to transform plant cells which are grown into plants that express the protein, specifically a Bacillus tharinglensis insecticidal crystal protein specifically a Bacillus centrally any protein that improves, nutritional value, imparts resistance to herbicides, pathogens or inhibits proteases, amylases or RNases. TES provide efficient cap and polyadenylation confidency while the use of a polymerase other than polyadenylation confidency that the polyadenylated RNA, whereas in current methods high yield expression of AT-rich genes is
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Van Aarssen R;
WPI; 98-077177/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimaeric gene providing high level expression of AT rich sequences in plants, useful for expressing insecticidal crystal proteins comprises promoter recognised by polymerase other than RNA polymerase II which generates uncapped mRNA including two viral
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Synthetic B. thuringiensis truncated crystal Chimaeric gene; plant cell transformation; insecticidal crystal protein; ICP; cry9C;
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21-JUN-1996; US-667731.
(PLBZ ) PLANT GENETIC S
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31-DEC-1997.
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V13119;
                               difficult
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                                                                   GTTCGCCGTGAACGGCCAGCAGGTGCCCCTGCTGAGCGTGTACGCCCAGGCCGTGAACCT
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ASSAVQHVNLLKEW	SDTDCPC	EDTDCPC	TAHTKN	GHRFCESCMAALLSSSSPKC	LQTNPPL LUTNPPL	99. 99. Live	sequen 104,'G' 1015637 1ger hou L; zinc Lnger h	finger	019260 (1) Bog	err vir	bach, M	(man) quence	LAP1		624 1607 886 944 1249 1816 389 669 829 1940	1957 1690 1974 791 1187 698
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SNSLEKKVSLLQNESVEKNKS		SCPHKCSVOTLLRSELSAHLSECVNA	RGCAEQLMI.GH-LYHLKNDCHFEELPCVRPDCKEKVIRKDLRDHVEKACKYREATCSHC 	SSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE                     SSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE	MESSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKTVEDKYKCEKCHLVL 	Score 2986.5; DB 2; Leng Pred. No. 4.6e-165; 0; Mismatches 1; Indel	t shown 568 <hua> :g595910; PIDN:AAA56753. Y gy <rng></rng></hua>	in interacts with the 5073988	:g675459; PIDN:AAA65732. M.S.; Dixit, V.M.	ansforming protein LMP1 5163092	lamanchili, R.; VanArsc	ng procein _revision 23-Mar-1995 #text_chan	, ii	ALIGNMENTS	X38418 X43212 H69378 H71404 H71404 S68960 S68960 7040809 T040809 T040809 T01362 T01362	
IQSLHNQICSFEI 299	FKRYGCV	N	ACKYREATCSHC 179              	EILALQIYCRNE 120          EILALQIYCRNE 120	DKYKCEKCHLVL 60	ngth 568; els 1; Gaps 1;	1; PID:g595911	cytoplasmic domain of CD40.	1; PID:g675460	engages signaling proteins	lale, T.; Ware, C.; Kieff, E.	hange 08-Oct-1999			probable zinc-bind insulin-like growt purine NTPase homo spindle pole body hypothetical prote laminin alpha-4 ch enamelin, 44K - bo hypothetical prote hypothetical prote hypothetical prote myosin heavy chain	hypothetical coile microtubule bindin hypothetical prote hypothetical prote hypothetical prote myosin heavy chain

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CD40 receptor-associated factor 1 - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 10-0
C; Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 10-0
C; Accession: A55960
R; Cheny, G; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltiscience 267, 1494 1498, 1995
Science 267, 1494 1498, 1995
A; Title: Involvement of CRAPI, a relative of TRAF, in CD40 signaling A; Title: Involvement of CRAPI, a relative of TRAF, in CD40 signaling A; Terence number: A55960; MUID:95184010
A; Accession: A55960
A; Accession: A55960
A; Residues: 1-568 < RES>
A; Cross-references: EMBL:U21092; NID:9726087; PID:9726088
C; Genetics:
A; Genetics: EMBL:U21092; NID:9726087; PID:9726088
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          EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR
                                                                            FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEI
                                                                                                                                               KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV
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Pred. No. 1e-164;
0; Mismatches 2;
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A; Molecule type: mRNA
A; Residues: 1-567 <RES>
A; Cross-references: EMBL:U21050; NID:97
C; Genetics:
A; Gene: CRAF1
C; Superfamily: RING finger homology
C; Keywords: zinc finger
F; 48-96/Domain: RING finger homology <R
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C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Nov-1999
C;Accession: 149772.
R;Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D. Science 267, 1494-1498, 1995
A;Title: Involvement of CRAFI, a relative of TRAF, in CD40 signaling.
A;Reference number: A55960; MUID:95184010
A;Accession: 149772.
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                                                   VTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIW
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95.6%;
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Pred. No. 1e-157;
7; Mismatches 16;
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CD40 receptor-associated protein CAP-1 - human (Species: Homo sapiens (man) (Date: 17-Jul-1998 #sequence_revision 17-Jul-1 (Accession: S68467; I53498 (Accession: S68467; I53498 (Accession: S68467; I53498 (Accession: S68467) (Accession: S68467) (Accession: S68467) (Accession: S68467)
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C;Keywords: homodimer; signal transduction;
F;49-97/Domain: RING finger homology <RNG>
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A:Experimental source: tissue-type fetal brain
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A; Residues: 1-543 <SAT>
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Best Local Similarity 94.0
Matches 539; Conservative
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                                                   KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG
                                                                                                                         EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRSFRQNWEEADSMKSSVESLQNR
                                                                                                                                                                                                            KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSE------
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                                         KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG
                                                                                  VTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIW
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Pred. No. 4.9e-155;
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A; Residues: 1-557 <MIZ>
A; Cross references: DDBJ: AB000509
C; Comment: This protein is involved
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C; Keywords: coiled coil; tumo
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R; Mizushima, S.; Fu
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Pred. No. 4.4e-61;
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R;Mizushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Otsuka, M.; Gene 207, 135-140, 1998
A;Title: Cloning and characterization of a cDNA encoding the human homolog of tumor A;Reference number: JC6539; MUID:98172745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor receptor-associated factor 5 homolog - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLEN--GTYIKDDTIFI
                                                                                                                                                                                                      GLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTL 437
                                                                                                                                                                                                                                                                                               SQAEKLKELIKEIRPF-----RQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNT
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LDQ-SGKKN;:METFKPDPNSSSFKRPDGEMNIASGCPRFVAHSVLENAKNAYIKDDTLFL
                                                                                                                                                                               AVLEEETNKHDTHINIHKAQLSKNEERFKLLEGTCYNGKLIWKVTDYKMKKREAVDGHTV
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INF receptor associated factor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-1
C;Accession: I61512
R;Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
Cell 78, 681-692, 1994
A;Title: A novel family of putative signal transducers associated w:
A;Reference number: A54750; MUID:94349371
A;Accession: I61512
A;Accession: I61512
A;Accession: I61512
A;Accession: I61512
A;Accession: I61512
A;Accession: I61512
A;Accession: I6513
A;Residues: 1-501 <RES>
A;Residues: 1-50
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tumor necrosis factor receptor-associated protein - W.Alternate names: TWF receptor-associated protein C.Species: Homo sapiens (man) C.Exte: 10-Oct-1995 #sequence_revision 01-Dec-1995 #c.Faccession: S56163; S58925; S58926
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R:Song, H.Y.; Donner, D. submitted to the EMBL Data A;Description: Association A;Reference number: $58925 A;Accession: $58925
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Biochem. J. 309, 825-829, 1995
A;Title: Association of a RING finger protein with the cytoplasmic domain A;Reference number: S56163; MUID:95366958
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C;Keywords: zinc finger
E;30-78/Domain: RING finger homology <RNG>
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A; Crestidues: 1-342, RPCAQCGHRYCSFCLASIL', 363-501 <SOF>
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C; Keywords: zinc finger
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                                             KDDTIFIKVIVDTSDL
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2000, 10:21:48 ; Search time 38.17 Seconds (without alignments) 460.331 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-224-556-2 3005 1 MESSKKMDSPGALQTNPPLK.....IKDDTIFIKVIVDTSDLPDP 567

Scoring table:

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85661 seqs, 30989116 residues

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85661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_38:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	J. B101. Chem. 269:30069-30072(1994).  -!- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS TO CO40 AND THE LYMPHOTOXIN-BETA RECEPTOR.  -!- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER THE RECEPTOR ASSOCIATED FACTORS (POTENTIAL).  -!- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.	FROM N 951296 Irie S member binds: 518: 518: 518: 518: 518: 518: 518: 518	FROM N.A. 95184010. Cleary A.M., Ye Z.S., Hong D.J. ent of CRAF1, a relative of TR 67:1494-1498(1995). FROM N.A., AND CHARACTERIZATION MPHOMA; 95163092. G., Birkenbach M., Yalamanchili G., Birkenbach M., Yalamanchili ein-Barr virus transforming pro for the tumor necrosis factor 1 89-399(1995).	

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EMBL; U15637; AAA56753.1; -.
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                                                                TVLENGTYIKDDTIFIKVIVDTSDLPDP
                                                                                                   EYDALLPWPFKQKYTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
                                                                                                                              KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG
                                                                                                                                                                   EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR
                                                                                                                                                                                                                                             SRGCAEQLMLGH-LVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHC
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                                                       TVLENGTYIKDDTIFIKVIVDTSDLPDP
                                                                                          EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
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PF00097; zf-C3HC4; 1.
TE; PS00518; ZINC_FINGER_C3HC4; finger; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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267
418
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         STANDARD;
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COILED COIL (POTENTIA
MATH/TRAF. 2 AND
MISSING (IN REF. 4).
MISSING (IN REF. 3).
P-> S (IN REF. 3).
P-> G (IN REF. 4).
R 6765533FBF523C8B CR
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Pred.
          PRT;
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ed. No. 1.2e-172;
Mismatches 2;
                                                       568
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"Y a concodes a TRAF-related protein.";

"Y encodes a TRAF-related protein.";

"Y encodes a TRAF-related protein.";

"Y encodes a TRAF-related protein.";

"Y color of the 177:274-290(1996).

"Y color of the 178.

"Y color of the 178.

"Y color of the LYMPOTOXIN-BETA RECEPTOR (TWY-R2). ALSO BINION THE LYMPOTOXIN-BETA RECEPTOR (BY SIMILARITY).

"Y COLOR OND THE LYMPOTOXIN-BETA RECEPTOR (BY SIMILARITY).

"Y COLOR OND THE LYMPOTOXIN-BETA THE THE THE RECEPTOR ALSO FOUND IN THE LYMPOTOXIN-BETA THE THE TIME THE TABLE OF OUND IN LYUER.

"Y ISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN LYUER.

"Y INDIET, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. IN FOUND IN LYUER.

"Y EMPLAYED BETWEEN EIL SAND EJS-CA.

"Y ENVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST LEVELS FOUND BETWEEN EIL SAND EJS-CA.

"Y SIMILARITY: CONTAINS A MATH-TRAF DOMAIN.
                                                                                                                  Query Match 95.1%;
Best Local Similarity 95.6%;
Matches 543; Conservative
                                                                                                                                                                                                                         EMBL; U21050; ÄAC52175.1; -.
EMBL; U31050; AAC52710.1; -.
MGD; MGI:108041; TRAF3;
PFAM; PF00917; MATH; 1.
PFAM; PF00917; MATH; 1.
PFAM; PF009518; ZINC_FINGER_C3HC4; 1.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
ZINC-finger; C6iled coil.
ZN_FING
C7 76 C3HC4-TXPE.
ZN_FING
C87 77 C0ILED COIL
DOMAIN
417 502 MATH/TRAF.
CONTELCT 72 73 CE -> WQ (IN)
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ZN_FING 2
DOMAIN 2
CONFLICT
CONFLICT :
SEQUENCE 5
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MEDLINE; 95184010.

Cheng G., Cleary A.M., Ye Z., Hong

'Involvement of CRAF1, a relative c

Science 267:1494-1498(1995).
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 96299439.
Wang X., Bornslaeg
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15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR (CRAF1) (TRAFAMN).
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                                                                        MESSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKTVEDKYKCEKCHLVL 60
CNPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQVYCRNE 119
            CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKKEILALQIYCENE 120
                                                      ; Metazoa; Chordata;
Eutheria; Rodentia;
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Disteche C.M.,
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TISSUE=BRAIN;
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                                                                                                                                                                                             C3HC4-TYPE.
COILED COIL (POTENT)
MATH/TRAF.
CE -> WQ (IN REF. 2).
T -> M (IN REF. 2).
W; 2522B343B41192DC C
                                                                                                                  Score 2859; I
Pred. No. 2.5e
7; Mismatches
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                                                                                                                   DB 1;
2.5e-165;
les 16;
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A novel family of putative signal transducers associated cytoplasmic domain of the 75 kDa tumor necrosis factor recell 78:681-692(1994).
                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2).
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01-FEB-1995
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                                                                                                                               SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
                                                                                                                                                                      SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR PROTEINS I AND 2 (IAPS), TO RECRUIT THEM TO THE TUMOR FACTOR RECEPTOR 2 (TNFR2).
                                                                                                                                                                                                                          FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TN ACTIVATES NF-KAPPA-B.
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AAC37662.1;
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                                                                                                                                                                                                                                       THE CYTOPLASMIC (TNF-R2) AND
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R OF APOPTOSIS
R NECROSIS
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RESULT
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Best Local Similarity
Matches 196; Conser
                                                                                 TRA2_HUMAN STANDARD;
TRA2_HUMAN STANDARD;
012933;
15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2) (TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger;
ZN_FING
DOMAIN
DOMAIN
SEQUENCE 50
                                                                                                                                                                                HUMAN
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PFAM; PF00917; MATH; 1.
PFAM; PF00997; Zf-C3HC4; 1.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                             Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
            MEDLINE;
                        SEQUENCE
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H.Y., Donner
                                                                                                                                                                                                                                                                                        NGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSS
                                                                                                                                                                                                                                                                                                                                      DMDLGFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYL
                                                                                                                                                                                                                                                                                                                                                                                                                      QILEQK-IATENIVCVLNREVER------VAVTAEACSRQHRLDQD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPKQTECGHRFCESCMAALLSSSSPKCTAC----QESI---VKDKVFKDNCCKREILA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKT-VEDKYKCEKCHLVLC
                                                                                                                                                                                                                             FQRPVSDMNTASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL
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           95366958
                        FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 828; DB 1;
Pred. No. 4.2e-43;
0; Mismatches 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATH/TRAF
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                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                          NECROSIS
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                                                                                                          FACTOR TYPE
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Matches 187
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PFAM; PF00917; MATH; 1.

PFAM; PF00997; zf-C3HC4; 1.

PROSITE; PS00518; ZINC_FINGER_C3HC4; 2

PROSITE; PS00518; ZINC_FINGER_C3HC4-TYP;
ZINC-FING 34 72

ZN_FING 34 72

DOMAIN 34 501

DOMAIN 34 501

DOMAIN 34 501

RPF2ACCH

CONFLICT 343 365
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"A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
Cell 78:681-692(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Association of a RING finger protein with the cytoplasmic domain the human type-2 tumour necrosis factor receptor."; piochem. J. 309:825-829(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND ACTIVATES NF-KAPPA-B.
SUBDNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS SUBDNIT: HOMODIMER OR HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPS), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).
SUBJECTIVILAR LOCATION: CYTOPLASMIC.
SUBJECTIVILAR LOCATION: CYTOPLASMIC.
SUBJECTIVILAR LOCATIONS A GENCY CLASS ZINC FINGER.
SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
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nes 187; Conserv
                370 GOVARNTGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIMKIRDYKRRKQ 429
                                                                                                       310
                                                                                                                                                                               261
                                                                                                                                                                                                                                                                                                                                                                     76 GIYEEGISILESSSAFPDNAARREVESLPAVC--PSDGCTWK---GTLKEYES-CHEGRC
                                                                                                                                                                                                                                                                                                                                                                                            SIVKDKV-----FKDNCCKREILALQIYCRNESRGCAEQLMLGHLVHLKNDCHFEEL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                              QPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE
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                                                                                                                                                                                                                  C-DGCGKKKIPREKFODHVKTCGKCRVPCRFHAIGCLETVEGEKQQ--EHEVQWLREHLA
                                                                                                                                                                                                                                                                                             PLMLTECPACKGLVRLGEKERHLEHECPERSLSCRHCRAPCCGADVKAHHEV-CPKFPLT
                                                                                                                                                                                                                                                                                                                               PCVR----PDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVS
                                                                                                                                                                           LLKEWSNSLEKK------VSLLQN-ESVEKNKSIQSLHNQICSFEIEIERQKEMLR
                                                                                                                                                                                                                                                      CPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV--FQGTNQQIKAHEASSAVQHVN
                                                                                                                                         ML--LSSVLEAKPLLGDQSHAGSELLQRCESLEKKTA--TFENIVCVLNREVER-----
                                                                                                     NNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 AA;
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MATH/TRAF.

RPFQAQCGHRYCSFCLASILRKL ->
LEMEASTYDGVFINKISDFARKR (IN

8883651EB6E20743 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             score 735.5; DB 1;
pred. No. 1.6e-37;
7; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C3HC4-TYPE.
-KDLAMADLEQKVRPFQAQCGHRYCSFCLASILKKLQ
                                                                            RQHRLDQD----KIEALSSKVQQLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 501;
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Best Local S
Matches 164
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Q13077;
Q15-FEB-2000
15-FEB-2000
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15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
THE RECEPTOR ASSOCIATED FACTOR 1 (TRAFI) (EPSTEIN-BARR VIRUS-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The Epstein-Barr virus transforming protein LMP proteins for the tumor necrosis factor receptor Cell 80:389-399(1995).
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SEQUENCE
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                                                                                 15
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                             PF00917; MATH; 1.
                                       PCVVVSCPHKCSVQTL-----LRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIK 248
                                                                                   ENEFPFGCPPTVCQDPKEP--
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                                                                                                                                                                                                                                                                 182
269
416
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
    -KCRGEDLQSISPGSRLRTQEKAH-PEVAEAGIGCPFAGVGCSFKGSPQSVQ 105
                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                         264
354
46163
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                                                                                                                                                                                          . 28
                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                         72;
                                                                                                                                                                    Score 637.5;
Pred. No. 9.9e
72; Mismatches
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Catarrhini; Hominidae;
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MATH/TRAF.
, A956A123A40D284A CRC64;
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or receptor family.";
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                                                                                              -RALCCAGCLSENP----RNGEDQIC
                                                                                                                                                                                            5; DB 1;
7.9e-32;
                                                                                                                                                                                 126;
                                                                                                                                                                                                                       Length
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                                                                                                         54
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                   Database :
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Maximum DB seq length: 2000000000
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Perfect score:
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SPTREMBL_12:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate
14: sp_unclassifi
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Gapop 10.0 , Gapext 0.5
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3005
1 MESSKKMDSPGALQTNPPLK.....IKDDTIFIKVIVDTSDLPDP 567
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_organelle:\*
sp\_phage:\*
sp\_plant:\*
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137.5	138	139	139	139.5	140	141	142	142	142	142.5	142.5	143	144	144.5	145	145	146.5	147	147.5	149		151.5	152	156	156.5
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## ALIGNMENTS

감	RA	RX	R K	RL	RT.	RT	RA:	R ?	R R	RN	RL	<b>7</b>	S E	3 5	RX	සි	RP	RN	RL	RT	RA	RX	RP :	RN	8	റ്റ	ည	GN	DE	H	DI	D	ğ ;	Š	1 T T T T T T T T T T T T T T T T T T T	RESULI	
TA novel kind ringer protein interacts with the cytopiasmic domain of CD40.";	H.M., O'ROURKE K., BOGUSKI M.S., DIXIT V.M.;	DLINE; 95073988.	[4] SEQUENCE FROM N.A.	t. 358:113-118(1995).	binds to the cytosolic domain of CD40.";	"A novel member of the TRAF family of putative signal transducing	IRIE S., REED J.C.;	MEDLINE: 95129692.	SEQUENCE FROM N.A.	[3]		proteins for the tumor necrosis factor receptor family.";	distribution the section and the two transfers	MOSTALOS G., BIRKENBACH M., YALAMANCHILI R., VANAKSDALE T., WARE C.,	95163092.	TISSUE=LYMPHOMA;	SEQUENCE FROM N.A., AND CHARACTERIZATION.	[2]	1-1498(1995).	lvement of CRAF1, a relative of TRAF, in CD40 signaling.";	CHENG G. CIFARY A.M. YE Z.S. HONG D. I. LEDERMAN S. BALTIMORE D.		SEQUENCE FROM N.A.		Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		1 OR CAP-1 OR CD40BP.	D PROTEIN) (LAP1).	ASSOCIATED FACTOR 3	12, Last annotation	TrEMBLIE 01	(TrEMBLrel	013114: 013076: 013947: 012940:	1211/ DDUTTWINNOV. DDW. SEO		

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BL; U19260; AAA65723.1; -.
BL; U15637; AAA68195.1; -.
BL; U15637; AAA56753.1; -.
4; 601896; -.
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                                                         TVLENGTYIKDDTIFIKVIVDTSDLPDP
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                                                                                                                                                          EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ 539
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                                                                                                                                    EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
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COILED COIL (POTENTIAL).
T-> M (IN REF. 2 AND 4).
MISSING (IN REF. 4).
MISSING (IN REF. 3).
P-> S (IN REF. 3).
P-> G (IN REF. 4).
R -> G (IN REF. 4).
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Pred. No. 2.3e-181;
0; Mismatches 2;
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FROM E14.5, ONLY LOW LEVELS ARE DETEC
-: SIMILARITY: CONTAINS A C3HC4-CLASS ZI
EMBL; U21050; AAC52175.1; -
EMBL; U33840; AAC52710.1; -
MGD; MGI:108041; Traf3.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
PFAM; PF00917; MATH; 1.
PFAM; PF00917; zf-C3HC4; 1.
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Q60803; Q62380;
Q1-NOV-1996 (TIEMBLIFEL 01, Created)
Q1-NOV-1996 (TIEMBLIFEL 01, Last sequence update)
Q1-NOV-1999 (TIEMBLIFEL 12, Last annotation update)
THE RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A candidate gene for the amnionless gastrulation encodes a TRAF-related protein.";
Dev. Biol. 177:274-290(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŚEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN-C57BL/6J; TISSUE-BRAIN;
MEDLINE; 96299439.
WANG X., BORNSLAEGER E.A., HAUB O., TOMIHARA-NEWBERGER C., LONBERG N.
DINULOS M.B., 'DISTECHE C.M., COPELAND N., GILBERT D.J., JENKINS N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 95184010.
CHENG G., CLEARY A.M., YE Z., HONG
"Involvement of CRAF1, a relative of Science 267:1494-1498(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRAF3 OR CRAF1 OR TRAFAMN.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS TO CDAO AND THE LYMPHOTOXIN-BETA RECEPTOR (BY SIMILARITY).

IF CUNCTION: MAY BE INVOLVED IN GASTRULATION.

IF SUBJURIT: HOMODIMER OR HETERODIMER WITH OTHER THE RECEPTOR ASSOCIATED FACTORS (POTENTIAL).

IT ISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT FOUND IN LIVER.

IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST IN DEVELOPMENTAL STACE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST
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KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV
                                                                                                                                                                 CNPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQVYCRNE
                                                                                                                                                                                             GRGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHC
                                                                                                 SRGCAEQLMLGH-LYHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHC
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                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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67 76
266 337
72 73
390 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C3HC4-TYPE.
COLLED COIL (POTENTIAL).
CC -> WQ (IN REF. 2).
T -> M (IN REF. 2).
T -> M CIN REF. 2).
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1.5 AND E13.5. AT
VELS ARE DETECTED.
                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                            Score 2859; DB 11;
Pred. No. 1.1e-173;
7; Mismatches 16;
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5. AT LATE
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signaling.";
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Mus.
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180

KSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV

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PRESULT POOL91
ID POOL91
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Best Local Similarity
Matches 243; Conserv
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01-FEB-1997
01-NOV-1999
TRAF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D83528; BAA11942.1; -.
MGD; MGI:107548; Traf5;
PROSITE; PS00518; ZINC_FINGER_C3HC4;
PPAM; PF00917; MATH; 1.
PPAM; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRAF5.
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-finger
SEQUENCE
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                           LG----HLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPM 185
                                                                                                                   RFCESCMAALLS-SSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNESRGCAEQLM 129
                                                                                                                                                                                        HSEEQAAVPCAFIRQNSGNSISLDFEPDTEYQFVEQLEERYKCAFCHSVLHNPHQTGCGH
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LGRFQDHLQH---
                                                                                          RFCQQCIRSLRELNSVPICPVDKEVIKPQEVFKDNCCKREVLNLHVYCKN-APGCNARII
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                                                                                                                                                                                                                                                                                                                                                                                                 558 AA;
                                                                                                                                                                                                                                                                                   Conservative
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-CSFQAVPCPNESCREAMLRKDVKEHLSAYCRFREEKCLYCKRDIVV
                                                                                                                                                                                                                                                                                                                                                                                                      64145 MW;
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                                                                                                                                                                                                                                                                                                      41.48;
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                                                                                                                                                                                                                                                                                Score 1244; DB 11;
Pred. No. 2e-71;
15; Mismatches 173;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 241
                                                                                                                                                                                                                                                                                                                                                                                         "TRAF5, an activator of NF-kappaB and put the lymphotoxin-beta receptor.";
J. Biol. Chem. 271:14661-14664(1996).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZI EMBL; D78141; BAA11218.1; -.

MGD; MGI:107548; Traf5
PROSITE; PS005:8; ZINC.FINGER_C3HC4; 1.
PFAM; PF00917; MATH; 1.
PFAM; PF00097; zf-C3HC4; 1.
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Q61480;
01-NOV-1996
01-NOV-1996
01-NOV-1999
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BALB/C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96278943.
  130
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nes 241; Conserv
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                                                RFCQQCIRSLRELNSVPICPVDKEVIKPQEVFKDNCCKREVLNLHVYCKN-APGCNARII 121
                                                                       RFCESCMAALLS-SSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNESRGCAEQLM 129
                                                                                                                                               HSEEQAAVPCAFIRQNSGNSISLDFEPDTEYQFVEQLEERYKCAFCHSVLHNPHQTGCGH
                                                                                                                                                                              HTDRSAGTP-VFVPEQGG------YKEKFVKTVEDKYKCEKCHLVLCSPKQTECGH 70
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                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                         64154 MW;
                                                                                                                                                                                                                                              41.4%; Score 1244; DB 11;
41.3%; Pred. No. 2e-71;
tive 113; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHUNG W.,
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Last annotation update)
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                                                            Query Match
Best Local Similarity
Matches .229; Conser
                                                                                                                                                                                                                                                                   MIZUSHIMA S., FUJITA M., ISHIDA T., AZUMA S., KAT
OTSUKA M., YAMAMOTO T., INOUE J.;
"Cloning and characterization of a cDNA encoding
tumor necrosis factor receptor associated factor
                                                                                                                                                                                                                                                                                                                                                                                         000463;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TRAF5 (TNF RECEPTOR ASSOCIATED FACTOR 5).
                                                                                                                                                         SEQUENCE OF 20-557 FROM N.A.

SEQUENCE OF 20-557 FROM N.A.

MEDLINE; 97321041.

MAKANO H., SHINDO M., YAMADA K., YOSHIDA M.C., SANTEE S.M., WARE (
JENKINS N.A., GILBERT D.J., YAGITA H., COPELAND N.G., OKUMURA K.;

"Human TNF receptor-associated factor 5 (TRAF5): CDNA cloning,
expression and assignment of the TRAF5 gene to chromosome 1q32.";

Genomics 42:26-32(1997).
                                                                                                                                                                                                                                                          Gene
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                         -!- SIMILARITY: CONTAINS A C3HC4-CLASS EMBL; AB000509; BAA25262.1; -. EMBL; U69108; AAC51329.1; -. PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     000463
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 98172745.
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                                                                                PFAM; PF00917; MATH; 1.
PFAM; PF00097; zf-C3HC4; 1.
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                                                                                                                                                                                                                                                           207:135-140(1998).
                                                               557
  Conservative
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-CSFQAVPCPNESCREAMLRKDVKEHLSAYCRFREEKCLYCKRDIVV
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                                                              64405
             39.3%;
                                                               WW;
  Score 1182; D
Pred. No. 1.7e
21; Mismatches
                                                               F46CAB2A
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               DB 4;
1.7e-67;
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                         Length 557;
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(TRAF5).";
                                                                                                                                                                                                                                                                                                          K., HIRAJ M.,
                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
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     20;
     Gaps
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01-JUN-1998 (TrembLrel. 06, Created)
01-JUN-1998 (TrembLrel. 06, Last sequence update)
01-NOV-1999 (TrembLrel. 12, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2A
                                                                                                                                 Tumor necrosis factor receptor (TNFR)-associated fa
a TRAF2 splice variant with an extended RING finger
inhibits TWRF2-mediated NF-kappaB activation.";
J. Biol. Chem. 273:4129-4134(1998).
-!- SIMILARITY: COMPAINS A C3HC4-CLASS ZINC FINGER.
EMBL; AF027570; AAC53545.1;
--- PROSITE: ES00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98129826.
BRINK R., LODISH H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6; TIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus
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                                                         PFAM; PF00917; MATH; 1.
PFAM; PF00097; zf-C3HC4; 1.
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Query Match
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Q12933;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-NOV-1999 (TrEMBLrel. 12, L
TUMOR NECROSIS FACTOR TYPE 2
                                                                                                                                                                                  MEDLINE; 953bby...
SONG H.Y., DONNER D.B.;
SONG H.Y., DONNER D.B.;
"Association of a RING finger protein
the human type-2 tumour necrosis factr
"ionhem. J. 309:825-829(1995).
SEQUENCE FROM N.A. SONG H.Y.; SUBmitted (JUL-1994)
                                                                           ROTHE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.;
"A novel family of putative signal transducers associated with cytoplasmic domain of the 75 kDa tumor necrosis factor receptor cell 78:681-692(1994).
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
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Last annotation update)
2 RECEPTOR ASSOCIATED PR
    EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                       ith the cytoplasmic
receptor.";
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                                                                                                  receptor.
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Query Match
Best Local
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Q13077;
Q13077;
Q13077;
Q13077;
Q11077;
Q1107071996 (TIEMBLTel. 01, Li
Q1-NOV-1996 (TIEMBLTel. 08, Li
Q1-NOV-1998 (TIEMBLTel. 08, Li
EPSTEIN-BARR VIRUS-INDUCED PR
HOMO Sapiens (Human),
Eukaryota; Metazoa; Chordata;
                                               SEQUENCE FROM N.A. TISSUE-LYMPHOID TUN MOSIALOS G., BIRKEN KIEFF E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS A C3HC4-CLASS EMBL; U12597; AAA87706.1; --
PROSITE; PS00518; ZINC_FINGER_C3HC4; 2.
PFAM; PF00917; MATH; 1.
PFAM; PF00097; zf-C3HC4; 1.
ZINC-finger.
Cell 0:0-0(0).
EMBL; U19261; AAA62309.1;
PFAM; PF00917; MATH; 1.
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                                                                                                                         Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGGYKEKFYKT-YEDKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC-QE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-DGCGKKKIPREKFQDHVKTCGKCRVPCRFHAIGCLETVEGEKQQ--EHEVQWLREHLA 245
                                                                                                                                                                                                                                                                                                                                RDDAIFIKAIVDLTGL
                                                                                                                                                                                                                                                                                                                                                    KDDTIFIKVIVDTSDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKS
: || :| :| :| :| :|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV--FQGTNQQIKAHEASSAVQHVN 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPGFSKTLLGTKLEAKYLCSACRNVLRRPFQAQCGHRYCSFCLASILSSGPQNCAACVHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187;
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                                                                                                                          Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                              BIRKENBACH
                                                                            TUMOR;
                                                                                                                         Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                      , Last sequence update) , Last annotation update) PROTEIN.
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                                                              YALAMANCHILI
                                                                                                                                                                                                                      Created)
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Pred. No. 2.7e-39;
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                                                                                                                                                                                                                                                       PRT;
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                                                              VANARSDALE
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                                                                                                                                           Mammalia;
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                                                              WARE
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SO

SEQUENCE

416

AA;

46163 MW;

760442EC CRC32;

Local Similarity

Conservative

72;

21.2%;

Score 637.5; DB 4; Pred. No. 3.5e-33; 2; Mismatches 126;

Length 416; Indels

103;

Gaps

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Best Local Sim
Matches 164;
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                                밁
                                                                                                                                               Query Match
Best Local 9
                                                                                                                            Matches 143;
                                               J.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PUTATIVE INTERLEUKIN 1 SIGNAL TRANSDUCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9Y4K3
Q9Y4K3;
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                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDILIR; 96434892.

CAO Z., XIONG J., TAKEUCHI M., KURAMA T., GOEDDE CAO Z., XIONG J., TAKEUCHI M., KURAMA T., GOEDDE CAO Z., XIONG J., TAKEUCHI M., KURAMA T., GOEDDE CAO Z., XIONG J., TAKEUCHI M., KURAMA T., GOEDDE CAO Z., VIONG J., TAKEUCHI M., KURAMA T., GOEDDE CAO Z., KURAMA T., KURAMA T., GOEDDE CAO Z., KURAMA T., GOEDDE CAO Z., KURAMA T., KURAMA T., GOEDDE CAO Z., KURAMA T., KURAMA T., GOEDDE CAO Z., KURAMA T., KUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292
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                                                                                                                                                                                                                                           Zinc-finger.
SEQUENCE 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLEQSIRLMEEASEDGTFLWKITNVTRRCHESACGRTVSLFSPAFYTAKYGYKLCLRLYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIVAVLNKEVE-----ASHLALATSIHQSQLDRERILSLEQRVVELQQTLAQKDQALG
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PMEEIOGYDVEFDPPLESKYECPICLMALREAVOTPCGHRFCKACIIKSIRDAGHKCPVD 108
                                                           FVPEQGGYKEKFVKTVEDKYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTAC
                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                522 AA;
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                                                                                                                                        101;
                                                                                                                                 Score 554.5; DB 4
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1; Mismatches 200
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                             REGNIER C.H., TOMASETTO C., MOOG-LUTZ C., CHENARD M.P., WENDLING C., RABASSET P., RIO M.C.;

RA BASSET P., RIO M.C.;

The presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of a new conserved domain in CART1, a novel member of the presence of the prese
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Q14848 PRELIMINARY; PRI; 4/0 AA.
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Q14848 PRI; 4/0 AA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TOMASETTO C., REGNIER C.H., MOOG-LUTZ C., MATTEI M.G., TOMASETTO, R.C., REGNIER C.H., MO.C.:
ILDEREAU R., BASSET P., RIO M.C.:
"Identification of four novel human genes amplified and "Identification of four novel human genes amplified and in breast carcinoma and localized to the q11-q21.3 region of the past carcinoma and localized to the q11-q21.3 regions of the past carcinoma.
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TISSUE-BREAST DERIVED METASTATIC LYMPH NODE;
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l or LAP1, strongly associates with the cytoplasmic C-terminal domain (M03148) of Epstein-Barr virus (EBV) latent infection membrane protein (H03148) of Epstein-Barr virus (EBV) latent infection membrane protein (LAP1), a domain that is stringently required for transformed cell growth. LAP1 is related to murine tumour necrosis factor receptor associated factor TRAF2. A related novel B-cell protein (M03147), EBI6, appears to be the human homologue of murine TRAF1. LAP1 polypeptides, esp. the LMP1 binding domain, coiled coil domain and c-terminal domain can be used to inhibit LMP1-TRAF interaction. Such polypeptides, which may be obtd. by recombinant means (see also T31273) can be used to treat infection and control cell growth or tumourigenesis associated with LMP1-encoding viruses, partic. EBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMP1 associated protein LAP1.

LAP1; LMP1 associated protein 1; latent infection membrane protein; tumour necrosis factor receptor associated factor; TRAF; signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AIDS; Hodgkin's disease; Burkitt's lymphoma; naspharyngeal carcinoma; mononucleosis; Epstein-Barr virus; EBV; therapy.
                                                                                                                                                                                                                              Compounds and methods for controlling TRAF-mediated signals -modulating interactions between Epstein Barr virus encoded pro LMP1, LAP1, TNF, TNFR to inhibit lymphoblast growth and
                                                                                                                                                                                                                                                                                                                                                                                11-JUL-1996.
28-DEC-1995; U16980.
30-DEC-1994; US-367540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W03146 standard; W03146;
                                                                                                                                                                                tumorigenesis.
Claim 74; Page 58-60; 87pp; English.
A novel human B-cell protein (W03146), termed LMPI associated protein
                                                                                                                                                                                                                                                                                 N-PSDB; T31273.
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77. MAR-1998 (first entry)
77. MAR-1998 (first entry)
77. MAR-1998 (first entry)
78. CPAPI-a (TRAF-3: p55; human;
78. WC CPAPI mediated intracellular signalling; organ rejection; allergy;
78. WC CPAPI mediated intracellular signalling; organ rejection; allergy;
79. WAR-1998 (first entry)
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Example 1: Fig 1D-0: 158pp; English.

This polypeptide comprises a CRAF1 (TRAF-3) protein designated CRAF1-a or TRAF-3-p55, p55, CRAF1(p55), TRAF-3(p55) or CRAF1(p60).

CRAF1-a or TRAF-3-p55, p55, CRAF1(p55), TRAF-3(p55) or CRAF1(p60).

CRAF1-a is a signalling protein that interacts with the cytoplasmic tail of B cell surface molecule CD40 and mediates a variety of T-dependent effects on B cell activation and differentiation. A higher mol.wt. CRAF1, designated CRAF1b (see W27429), p15 (see W27430) and variants of CRAF-1a and CRAF-b (see W27432-37) that comprising from 0-4 zinc finger domains, and nucleic acids encoding them, can be used to inhibit CD40 ligand activation of cells that express CD40 on their surface, particularly by introducing the nucleic acid molecule into the cells, useful to treat conditions characterised by an aberrant or unwanted level of CD40 mediated intracellular signalling, such as organ rejection, or a CD40 dependent immune response in a subject receiving gene therapy. The condition may be dependent on CD40 ligand-induced activation of epithelial or an interactivation of college of the may be dependent on CD40 ligand-induced activation of epithelial or an interactivation of college.
                                                                                                                                                                              Query Match
Best Local S
Matches 565
                                                                                                                                                                                                                                                                              cells, an inflammatory kidney disease, a smooth muscle cell-
dependent disease, or a condition associated with Epstein-Barr
virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein comprising CRAFI-b domain capable of inhibiting CD40 mediated cell activation - useful to treat conditions characterised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1996; US-016659.
(UYCO ) UNIV COLUMBIA NEW YORK.
Cleary AM, Frank DM, Lederman S
WPI; 97-479907/44.
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21-MAR-1999; US-026584.
18-SEP-1996; US-013820.
21-MAR-1996; US-013820.
01-MAY-1996; US-016626.
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25-SEP-1997.
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                                                                                                                                                                                Local Sin
hes 565;
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SRGCAEQLMLGH-LVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHC
                                                                                                           MESSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKTVEDKYKCEKCHLVL 60
                                              CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cys-208,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e- "zinc finger 1 (Zn binding to Cys-117,
Cys-124, His-136 and Cys-141)"
.170
                                                                                                                                                                                             99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e= "zinc finger 2 (zinc binding to Cys-148
Cys-153, His-165 and Cys-170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "zinc finger 5 (Zn binding to Cys-232, Cys-239, His-251 and 259-381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "zinc finger 4 (Zn binding to Cys-204
Cys-208, His-221 and Cys-225)"
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                                                                                                                                                                                <u>.</u>
                                                                                                                                                                            Score 2980.5; DB 1;
Pred. No. 8.9e-227;
D; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
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His-192 a
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and Cys-197"
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DE Human CRAF1-b (TRAF-3-p70) polypeptide.

WCD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;

KW CD40 mediated intracellular signalling; organ rejection; allergy;

KW hay fever; autoimmune disease; systemic lupus erythematosus;

KW disease; militus; psoriasis; hyper immunojobulin E syndrome;

KW disease; Rieter's syndrome; spondyloarthritis; Lyme disease; HIV;

KW apoptosis; Rieter's syndrome; sung; hepatitis; cirrhosis;

KW syphilis; tuberculosis; farmer's lung; hepatitis; cirrhosis;

KW pneumoconiosis; adult respiratory distress syndrome; pneumonitis;

KW asbestosis; siliconosis; farmer's lung; hepatitis; cirrhosis;

KW glomerulosclerosis; glomerulopathy; kidney disease; nephropathy;

KW disease; heprosy; malaria; Goodpasture's disease;

KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;

Wegener's granulomatosis; cryoimmunoglobulinaemia;

KW Waldenstroem's macroglobulinaemia; amyloidosis; Sjogren's sydrome;

Waldenstroem's macroglobulinaemia; amyloidosis; Sjogren's sydrome;
                  Region
                                                                      Region
                                                                                                                         Region
                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                         AIDS; oesophageal dysmotility; inflammatory bowel disease; bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour; Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541
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                                                                                                                                                                                                                                                                                            therapy;
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                                                                                                                                                                                                                                                                                            diagnosis.
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239. .2
                                                                                                                             270.
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                     /note-
                                                                                                                                                                 /note-
                                                                                                                                                                                                 /label= CRAF-b_domain
/note= "Claim 1"
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                 . 263
                                                                                                                             . 292
"zinc finger 4 (Zn binding to Cys-326,
                                                                                                                                          "zinc finger 1 (Zn binding to Cys-239, Cys-246, His-258 and Cys-263)"
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330, His-343 and Cys-347)"

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Figura
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein comprising CRAF1-b domain capable of inhibiting CD40 mediated cell activation - useful to treat conditions characterised by aborrant or unwanted level of CD40 mediated intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-1996; US-013820.
01-MAY-1996; US-016626.
01-MAY-1996; US-016626.
01-MAY-1996; US-016626.
(UYCO ) UNIV COLUMBIA NEW YORK.
Cleary AM, Frank DM, Lederman S;
WPI; 97-479907/44.
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                                                                                                                                                                                                                                                                                                                                                                                          MESSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKTVEDKYKCEKCHLVL 182
                                      SRGCAEQLMLGH-LVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREAICSHC
  EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR
                                                                                                                             KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV 239
                                                                                                                                                                                                                  SRGCAEQLTLGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHC
                                                                                                                                                                                                                                                                                                     CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE
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/note= "
44. .47
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103. .11
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Pred. No. 1.2e-226;
0; Mismatches 2;
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DE Human CRARI isoform p55deig)

EXW CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human; KW CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human; KW CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human; KW CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human; KW CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human; KW cD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human; KW hay fever; autoimmune disease; systemic lugus erythematosus; KW rheumatoid arthritis; myasthenia gravis; Graves' disease; KW alopathic thrombocytopaenia purpura; haemolytic anaemia; KW approssis; Raleter's syndrome; spondyloarthritis; Lyme disease; HIV; KW approssis; adult respiratory distress syndrome; pneumonitis; KW approsociatis; siliconosis; Farmer's lung; hepatitis; cirrhosis; KW absestosis; siliconosis; Farmer's lung; hepatitis; cirrhosis; KW alomerulosclerosis; plomerulopathy; kidney disease; nephropathy; KW endocarditis; leprosy; malaria; Goodpasture's disease; Henoch-Schoenlein purpura; polyarteritis; multiple myeloma; KW Waldenstroem's macroglobulinaemia; amyloidosis; Sjogren's sydrome; KW Waldenstroem's macroglobulinaemia; amyloidosis; Sjogren's sydrome; KW AIDS; oesophageal dysmotility; inflammatory bowel disease; bibliomerulinaemia; namyloidosis; B cell tumour; contributed to the process of the process of
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                                                                                                                      WO9734473-A1.
25-SEP-1997; U05076.
21-MAR-1997; US-026584.
18-SEP-1996; US-013820.
21-MAR-1996; US-016626.
01-MAY-1996; US-016626.
01-MAY-1996; US-01659.
(UYCO) UNIV COLUMBIA NEW YORK.
Cleary AM, Frank DM, Lederman S;
WPI; 97-479907/444.
Protein comprising CRAFI-b domain capable of inhibiting CD40 mediated cell activation - useful to treat conditions charact by abstrant or unwanted level of CD40 mediated intracellular signalling Example 1; Fig iD-O; 158pp; English.
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27-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                           N-PSDB; T90123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "zinc finger 1 (2n binding to
Cys-124, His-136 and Cys-141)
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CC This polypeptide comprises a CRAFI (TRAF-3) isoform designated p55del9. It is encoded by exons 4-8 and 10-13 of the human CRAF CC gene (see T90123) and arises by alternative splicing of the sequence for CRAFI-a (see W27431), a signalling protein that CC interacts with the cytoplasmic tail of B cell surface molecule CD40 and which mediates a variety of T-dependent effects on B cell activation and differentiation. A higher mol.wt. CRAFI, designated CC CRAFIb (see W27428), has also been identified, as well as isoforms CC CRAFIb (see W27428), p15 (see W27430) and variants of CRAFI and CC CRAFIb (see W27432-37) that comprise different combinations of 5 clic fingers. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC companies. CRAFI peptides, comprising from 0-4 zinc finger CC cand used to treat conditions characterised by an aberrant or CC companies to CD40 mediated intracellular signalling, such as corgan rejection, or a CD40 dependent immune response in a subject receiving gene therapy. The condition may be an allergic response or an autoimmune response, or may be dependent on CD40 ligand-induced activation of epithelial cells, an inflammatory kidney disease, a smooth muscle cell-dependent disease, or a condition cascolated with Epstein-Barr virus.
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                        TVLENGTYIKDDTIFIKVIVDTSDLPDP
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                                                            EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ 539
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RESULT W27433 ID W2

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W27433 standard; Protein; 665 AA.

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DT 27-MA-1998 (first entry)

DE Human CRAF1-b isoform p70del9.

WCD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human; KW CD40 mediated intracellular signalling; organ rejection; allergy; KW CD40 mediated intracellular signalling; organ rejection; allergy; KW cD40 mediated intracellular signalling; organ rejection; allergy; KW hay fever; autoimmune disease; systemic lupus erythematosus; KW rheumatoid arthritis; myasthenia gravis; Graves' disease; KW hay fever; autoimmune disease; systemic lupus erythematosus; KW diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome; Syndrome; spondyloarthritis; Lyme disease; HIV; KW apoptosis; Rieter's syndrome; spondyloarthritis; Lyme disease; HIV; KW apoptosis; Rieter's syndrome; pneumonitis; KW apoptosis; adult respiratory distress syndrome; pneumonitis; KW pneumoconiosis; adult respiratory distress syndrome; pneumonitis; KW asbestosis; sliiconosis; Farmer's lung; hepatitis; cirrhosis; KW atherosclerosis; glomerulopathy; kidney disease; nephropathy; KW glomerulosclerosis; glomerulopathy; kidney disease; nephropathy; KW endocarditis; leprosy; malaria; Goodpasture's disease; KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma; KW Wegener's granulomatosis; cryoimmunoglobulinaemia; KW Wegener's macroglobulinaemia; amyloidosis; Sjogren's sydrome; KW Milos; oesophageal dysmotility; inflammatory bowel disease; betternev; disease; Epstein-Barr virus; mononucleosis; B cell tumour; KW Butkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
Example 1; Fig 1A-0; 158pp; English.

CThis polypeptide comprises a CRAF1 (TRAF-3) protein designated protein tis encoded by exons 1-2, 4-8 and 10-13 of the human protein gene (see T9013). Different isoforms (W77428-37) of CRAF1 CRAF1 (TRAF gene (see T90123). Different isoforms (W77428-37) of CRAF1 craft protein gene designation of the models comprising from 0-4 zinc finger domains, and nucleic acids encoding them, can be used to inhibit CD40 ligand activation of cells that express CD40 on their surface, particularly by introducing the nucleic acid molecule into the cells, and used to treat conditions characterised by an abserrant or unwanted level of CD40 mediated intracellular signalling, such as organ rejection, or a cD40 dependent immune response in a subject recealving gene therapy. The condition may be an allergic response or an autoimmune response, or may be dependent on CD40 ligand-induced activation of epithelial cells, an inflammatory kidney disease, a
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25-SEP-1997.
21-MAR-1997; U
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01-MAY-1996; U
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27-MAR-1998 (
Human CRAF1-b
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/note= "Claim 1"
239. .263
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Cys-246, His-258 and Cys-263)"
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with Epstein-Barr virus.
Sequence 665 AA;
WO9616665-A1.
06-JUN-1996.
04-DEC-1995; U15695
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CD40 associated prot
cell proliferation;
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23-MAR-1998 (first entry)
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117. .141
/note= "Z
148. .170
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protein; CAP; ag
ion; treatment; c
                                                                                                             /note=
177. .1
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ed. No. 4.9e-214;
Mismatches 2;
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autoimmune disease.
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RESULT W27436 ID W AC W DT 2

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PS Claim 3; Fig 1; 94pp; English.

C This is a CD40 associated protein (CAP)-1. This CAP is a protein that specifically binds to CD40, a cell surface receptor involved in apoptosis. Agonists and antagonists of CAP can increase or decrease the level of CAP expression in a cell and can thereby modulate the function of the cell. Such compounds can be used to treat cancer, autoimmune diseases like asthma, hay fever, rheumatoid arthritis and immunodeficiency diseases and neurodegeneration. Antibodies that bind specifically to CAP can be used to assay CAP, to detect pathologically caltered levels. The encoding nucleic acid can be used to identify crelated genes and to express CAP for gene therapy.
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Best Local Similarity
Matches 538; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1994; US-349
(LJOL-) LA JOLLA CA
Reed JC, Sato T;
WPI; 96-286818/29.
N-PSDB; T30773.
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TVLENGTYIKDDTIFIKVIVDTSDLPDP
                       TVLENGTYIKDDTIFIKVIVDTSDLPDP
                                                                            EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
                                                                                                                       KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG
                                                                                                                                                                                                                                                          EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR
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                                                                                                                                                                                                                                                                                                                                                                             KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MESSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKTVEDKYKCEKCHLVL
                                                                EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
                                                                                                                                                                                                                                           EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRSFRQNWEEADSMKSSVESLQNR
                                                                                                                                                                                                                                                                                                     --GTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEI
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Pred. No. 6.6e-7
0; Mismatches
       543
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.6e-213;
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Example 1; Fig 1A-O; 158pp; English.

Example 1; Fig 1A-O; 158pp; English.

This polypeptide comprises a CRAFI (TRAF-3) protein designated produced by exons 1-2, 4-7 and 10-13 of the human provided by exons 1-2, 4-7 and 10-13 of the human CRAFI gene (see T90123). Different isoforms (W27428-37) of CRAFI craft produced produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D 25-SEP-1997.

121-MAR-1997; U05076.

R 18-SEP-1996; U5-026584.

R 21-MAR-1996; U5-026584.

R 21-MAY-1996; US-013820.

R 01-MAY-1996; US-016626.

R 01-MAY-1996; US-016659.

R 1997; 97-479907/44.

R-PSDB; T90123.

PT Protein comprising CRAF1-b domain capable of inhibiting CD40 mediated cell activation - useful to treat conditions characterised by aberrant or unwanted level of CD40 mediated intracellular aircallular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD40 receptor associated factor 1; CRAFI-b; TRAF-3; p70; human; CD40 mediated intracellular signalling; organ rejection; allergy; hay fever; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; Graves disease; indicated introduction and gravis; Graves disease; indicated arthritis; myasthenia gravis; Graves disease; indicated arthritis; psoriasis; hyper immunoglobulin E syndrome; gravis; gravis; gravis; indicated arthritis; psoriasis; hyper immunoglobulin E syndrome; gravis; indicated arthritis; scleroderma; pulmonary fibrosis; ppolyholis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis; pneumoconiosis; alliconosis; farmer's lung; hepatitis; cirrhosis; pneumoconiosis; farmer's lung; hepatitis; cirrhosis; indicated arthritis; glomerulonephritis; indicated arthritis; glomerulopathy; kidney disease; nephropathy; widnerdidits; leprosy; malaria; Goodpasture's disease; melmocratis; granulomatosis; granulomatosis; cryoimmunoglobulinaemia; welcone; walder disease; psyein Barr virus; monopucleosis; Begil tumour; polyarteritis; multiple myelome; plantiff a lamphome; psyein Barr virus; monopucleosis; gell tumour; procedured and sease; psyein Barr virus; monopucleosis; Begil tumour; procedured and sease; psyein Barr virus; monopucleosis; gell tumour; procedured and sease; psyein Barr virus; monopucleosis; gell tumour; procedured and sease; psyein Barr virus; monopucleosis; gell tumour; procedured and sease; psyein Barr virus; monopucleosis; psyein tumour; procedured and sease; psyein Barr virus; monopucleosis; psyein tumour; procedured and sease; psyein Barr virus; monopucleosis; psyein tumour; procedured and sease; psyein Barr virus; monopucleosis; psyein tumour; procedured and sease; psyein Barr virus; monopucleosis; psyein tumour; psyein t
                                                             smooth muscle cell-dependent
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/note= "Claim 1"
239. .263
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103. .1
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                                 virus.
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Cys-275, His-287 and Cys-292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "zinc finger 1 (zn binding to Cys-239, Cys-246, His-258 and Cys-263)"
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                                                                   disease,
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Query Match

.38;

Score 2652.5;

DВ

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Length

516;

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WARNER OF THE POST OF THE POST
                                                                                                                                                                       E Human CARRI-by (LIISL WILLY)

E Human CARRI-b isoform p70del8,9.

W CD40 receptor associated factor 1; CRAFI-b; TRAF-3; p70; human;

W CD40 mediated intracellular signalling; organ rejection; allergy;

W hay fever; autoimmune disease; systemic lupus erythematosus;

W rheumatoid arthritis; myasthenia gravis; Graves' disease;

W idiopathic thrombocytopaenia purpura; haemolytic anaemia;

W idiopathic thrombocytopaenia purpura; haemolytic anaemia;

W idiopathic thrombocytopaenia; purpura; pulmonary fibrosis;

W gapoptosis; Rieter's syndrome; spondyloarthritis; Lyme disease; HIV;

W syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;

W syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;

W syphilis; tuberculosis; Farmer's lung; hepatitis; cirrhosis;

W syphilis; tuberculosis; Farmer's lung; hepatitis; cirrhosis;

W asbestosis; siliconosis; Farmer's lung; hepatitis; cirrhosis;

W atherosclerosis; multiple sclerosis; glomerulonephritis;

W atherosclerosis; multiple sclerosis; glomerulonephritis;

W atherosclerosis; polyarerulopathy; kidney disease; nephropathy;

W endocarditis; leprosy; malaria; Goodpasture's disease;

W wegener's granulomatosis; cryolmmunoglobulinaemia;

W wegener's granulomatosis; cryolmmunoglobulinaemia;

W wegener's macroglobulinaemia; amyloldosis; Sjogren's sydrome;

W wldenstroem's macroglobulinaemia; amyloldosis; Sjogren's sydrome;

W waldenstroem's macroglobulinaemia; amyloldosis; Sjogren's sydrome;

W wegener's granulomatospy bowel disease;
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                                                                    Homo sapiens
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                                                                                                                                                             oesophageal dysmotility; inflammatory bowel disc
er disease; Epstein-Barr virus; mononucleosis; B
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Location/Qualifiers 52. .122
                                                                                                                              nasopharyngeal carcinoma;
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Example 1; Fig 1A-O; 158pp; English.

CC This polypeptide comprises a CRAFI (TRAF-3) protein designated ps This polypeptide comprises a CRAFI (TRAF-3) and 10-13 of the human CC prodels, 9 that is encoded by exons 1-2, 4-7 and 10-13 of CRAFI CC (RAF gene (see T90123). Different isoforms (W27428-37) of CRAFI CC (RAF gene (see T90123). Different isoforms with splicing. CRAFI CC encoding them, can be used to inhibit CDA0 ligand activation of CC cells that express CD40 on their surface, particularly by cells that express CD40 on their surface, particularly by CC (CC introducing the nucleic acid molecule into the cells, and used to CC treat conditions characterised by an aberrant or unwanted level of CC (treat conditions characterised by an aberrant or unwanted level of CC (CD40 mediated intracellular signalling, such as organ rejection, or CC (CD40 mediated intracellular signalling, such as organ rejection, or CC actoration of epithelial cells, an inflammatory kidney disease, a crivation of epithelial cells, an inflammatory kidney disease, a smooth muscle cell-dependent disease, or a condition associated contractors.
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25-SEP-1997; U05076.
21-MAR-1997; U05076.
18-SEP-1996; US-016584.
18-SEP-1996; US-01626.
01-MAY-1996; US-016629.
01-MAY-1996; US-016659.
01-MAY-1996; US-016659.
(UYCO) UNIV COLUMBIA NEW YORK.
(UYCO) UNIV COLUMBIA NEW YORK.
CLEATY AM, Frank DM, Lederman S;
WPI; 97-479907/44.
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Best Local Similarity
Matches 513; Conser
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Protein comprising CRAFI-b domain capable of inhibiting CD40 protein comprising crarion - useful to treat conditions characterised mediated cell activation - useful to treat conditions characterised by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular
                                                                                                                                                             183
                                                                                                                                                                                                                 123
                                                      303
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                                                                                                          243
                                                                                                                                    121
                            240
                                                                                                                                                                                        51
                                                                                                                                                                                                               Epstein-Barr virus.
                                                                                                                                                           KSOVEMIALOKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV
                                                        KSQVPMIAL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "putative 5
103. .110
/note="""
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/note= "Claim 1"
239 . 263
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44. 47
/note-
103. .1
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "zinc finger 1 (Zn binding to Cys-239, Cys-246, His-258 and Cys-263)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "putative SH3 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "zinc finger 2 (zinc binding to Cys-270, Cys-275, His-287 and Cys-292"
                                                                                                                                                                                                                                                                                       90.3%;
                                                                                                                                                                                                                                                                            score 2652.5; DB 1;
pred. No. 7.1e-201;
0; Mismatches 2;
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                PRESCRIPTION OF THE PROPERTY O
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AC 27-MAR-1998 (first entry)
DT Human CRAF1 isoform p55del9,10.
DE Human CRAF1 isoform p55del9,10.
DE Human CRAF1 isoform p55del9,10.
ED Human CRAF1 isoform p55del9,10.
DE Human CRAF1
PF 21-MAR-1997; U05076.

PR 18-SEP-1996; US-0136584.

PR 21-MAR-1996; US-013620.

PR 01-MAY-1996; US-013659.

PR (UYCO) UNIV COLUMBIA NEW YORK.

PI Cleary AM, Frank DM, Lederman S;

PI Cleary AM, Frank DM, Lederman S;

PI PROBB; T90123.

DR N-PSDB; T90123.

DR N-PSDB; T90123.

PR Protein comprising CRAF1-b domain capable of inhibiting CD40

PT mediated cell activation - useful to treat conditions characterised producted cell activation - useful to treat conditions characterised producted cell activation - useful to treat conditions characterised by aberrant or unwanted level of CD40 mediated intracellular producted intracellular by aberrant or unwanted level of CD40 mediated intracellular producted intracellular by aberrant or unwanted level of CD40 mediated intracellular producted intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant or unwanted level of CD40 mediated intracellular by aberrant by aberrant or unwanted level of CD40 mediated intracellular by aberrant by a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note- "zinc finger 2 (zinc t
Cys-153, His-165 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "zinc finger 1 (Zn Cys-124, His-136 a 148. .170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "zinc finger 3 (Zn binding to Cys-177, Cys-180, His-192 and Cys-197"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n binding to Cys-117, and Cys-141)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding to
d Cys-170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cys-148,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430
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PS Example 1; Fig 1D-0; 158pp; English.

CC This polypeptide comprises a CRAF1 (TRAF-3) isoform designated CC p55del9; 10. It is encoded by exons 4-8 and 11-13 of the human CC CRAF gene (see T90123) and arises by alternative splicing of the sequence for CRAF1-a (see W27431), a signalling protein that CC interacts with the cytoplasmic tail of B cell surface molecule CD40 and which mediates a variety of T-dependent effects on B cell CC arctivation and differentiation. A higher mol.wt. CRAF1, designated CC CRAF1b (see W27428), has also been identified, as well as isoforms CC picker (see W27432-37) that comprise different combinations of 5 czinc fingers. CRAF1 peptides, comprising from 0-4 zinc finger CC companis, and nucleic acids encoding them, can be used to inhibit CC particularly by introducing a nucleic acid molecule into the cells, and used to treat conditions characterised by an aberrant or CC unwanted level of CD40 mediated intracellular signalling, such as organ rejection, or a CD40 dependent immune response in a subject receiving gene therapy. The condition may be an allergic response or an autoimmune response, or may be dependent on CD40 ligand-culsed activation of epithelial cells, an inflammatory kidney collaborated with Epstein-Barr virus.
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Best Local Similarity
Matches 509; Consert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRGCAEQLMLGH-LVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE
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                     TVLENGTYIKDDTIFIKVIVDTSDLPDP
                                                                                                                            EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
                                                                                                                                                                                                 KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG
                                                                                                                                                                                                                       KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG
                                                                                                                                                                                                                                                                                                    VTELESYDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIW
                                                                                                                                                                                                                                                                                                                            VTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIW
                                                                                                                                                                                                                                                                                                                                                                                                         EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR
                                                                                                                                                                                                                                                                                                                                                                                                                                   EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRGCAEQLTLGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHC
                                                                                                  EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2646.5; DB 1;
Pred. No. 1.6e-200;
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Example 1; Fig 1A-O; 158pp; English.

CC This polypeptide comprises a CRAFI (TRAF-3) protein designated CC This polypeptide comprises a CRAFI (TRAF-3) protein designated CC prodel9; 10 that is encoded by exons 1-2, 4-8 and 11-13 of the human CC prodel9; 10 that is encoded by exons 1-2 and include CRAFI CC peptides comprising from 0-4 zinc finger domains, and nucleic acids encoding them, can be used to inhibit CD40 ligand activation of CC cells that express CD40 on their surface, particularly by cells that express CD40 on their surface, particularly by crat conditions characterised by an aberrant or unwanted level of CD40 mediated intracellular signalling, such as organ rejection, or a CD40 dependent immune response in a subject receiving gene cutherapy. The condition may be an allergic response or an autoimmune response, or may be dependent on CD40 ligand-induced
                                                                CD40 receptor associated factor 1; CRAFI-b; TRAF-3; p70; human; CD40 mediated intracellular signalling; organ rejection; allergy; Whay fever; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; Graves' disease; syndrome; disease; syndrome; syndrome; haemolytic anaemia; diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome; which is syndrome; syndrome; spondyloarthritis; Lyme disease; HIV; syphilis; tube; culosis; arthritis; scleroderma; pulmonary fibrosis; which is syndrome; syndrome; phemonary fibrosis; when preumoconiosis; adult respiratory distress syndrome; pneumonitis; when shestosis; siliconosis; Farmer's lung; hepatitis; cirrhosis; where society siliconosis; farmer's glomerulonephritis; when cheschesis; multiple sclerosis; glomerulonephritis; multiple sclerosis; goodpasture's disease; mephropathy; when coh-Schoenlein purpura; polyarteritis; multiple myeloma; wegener's granulomatosis; cryoimmunoglobulinaemia; Sjogren's sydrome; when coh-Schoenlein purpura; polyarteritis; multiple myeloma; sydrome; sydrome; sydrome; sydrome; sydrome; sydrome; sydrome; syd
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21-MAR-1997;
18-SEP-1996;
21-MAR-1996;
01-MAY-1996;
01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                         Protein comprising CRAF1-b domain capable of inhibiting CD40 mediated cell activation - useful to treat conditions characterised by aberrant or unwanted level of CD40 mediated intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 97-479907/44.
N-PSDB; T90123.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS; oesophageal dysmotility; inflammatory bowel disease; bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour; Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CRAF1-b
CD40 receptor
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W27435;
27-MAR-1998 (fin
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US-013820.
US-016626.
US-016659.
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52. 122
/label- CRAF-b_domain
/note= "Claim 1"
239. 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "zinc finger 2 (zinc binding to Cys-270,
Cys-275, His-287 and Cys-292 "
299 .319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
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.110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "zinc finger 1 (2n binding to Cys-239, Cys-246, His-258 and Cys-263)"
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Best Local S
Matches 509
                                                                                                                                                                                                                                                                                                    R98835 standard; Protein; 4;
R98835;
23-MAR-1998 (first entry)
CD40 associated protein; CAN
CD40 associated protein; CAN
                                                                                                                                                                                                                          cell proliferation; Homo sapiens. WO9616665-Al. 06-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activation of epithelial cells, an inflammatory kidney disease, smooth muscle cell-dependent disease, or a condition associated with Epstein-Barr virus.
New CD40 associated protein, agonists and antage modulate cell proliferation, immune response, a for treating cancer or autoimmune disease Claim 5; Page -; 94pp; English. This is a clone of the CD40 associated protein pSK-7 encodes amino acids 82 to 543 of CAP-1. I
                                                                                                                                               04-DEC-1995; U15695.
02-DEC-1994; US-349357.
(LJOL-) LA JOLLA CANCER
Reed JC, Sato T;
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96-286818/29.
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                                                                                                                                                                                                                                                                                   protein (CAP)-1 clone pSK-7 (residues 82-543).
protein; CAP; agonist; antagonist; gene therapy;
ion; treatment; cancer; autoimmune disease.
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Pred. No. 2.1
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The CAP sp
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Best Local S
Matches 467
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Note: This sequence of been created from the sequence 472 AA;
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                                                                                                                                18-MAR-1998 (first entry)
Murine TRAF5, a novel TNF receptor associated
TRAF5; tumour necrosis factor receptor; TNF;
TNF signal transducer system.
            (SUME) SUMITOMO ELECTRIC Nakano H, Nakata M, Okumur WPI; 97-435162/40.
N-PSDB; T87039.
                                                                W09731110-A1.
28-AUG-1997.
24-FEB-1997; J00512.
22-FEB-1996; JP-034574.
                                                                                                                                                                        W29257;
18-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                        VMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQ
                                                                                                                                                                                                                                                                                                                                                                                       VMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQ 491
                                                                                                                                                                                                                                                                                                                                                                                                                            QVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEA
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                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                  Protein;
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                                         Okumura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.4%;
                                                                                                                                                                                                                                                                                             567
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Pred. No. 2e-1
0; Mismatches
                                   (, Yagita
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2416; DB 1
No. 2e-182;
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                           Mus sp.
W09738099-A1.
16-OCT-1997.
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The present sequence represents a novel protein, designated TRAF5, which is a member of the tumour necrosis factor (TNF) receptor associated factor family. The TRAF5 protein has a coiled-coil domain, a leucine zipper motif and binds to lymphotoxin beta receptor and to CD30, but not to CD40 or TNF receptor 2. TRAF5 and its corresponding DNA are useful for the investigation of the signal transducer system of the TNF receptor family and the functions of TRAF proteins. They can also be used as probes for research and diagnostic purposes, and investigation of the specific applications of potential therapeutic agents.

Sequence 558 AA;
                                                                                                       Murine; mouse; TRAF5; tumour necrosis factor; TNF; allergy; receptor associated factor family; immunisation; treatment; cell proliferation inhibitor; screening; inhibitor; regulator.
                                                                                                                                                                                                                                    27-APR-1998
                                                                                                                                                                                                        Murine TRAF5
                                                                                                                                                                                                                                                                                              W27609 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LG----HLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMNIASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDTSDLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRSLVDAVDSVKQRITQLEASD-----QRLVLLEGETSKHDAHINIHKAQLNKNEERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFCESCMAALLS-SSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNESRGCAEQLM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSEEQAAVPCAFIRQNSGNSISLDFEPDTEYQFVEQLEERYKCAFCHSVLHNPHQTGCGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQ
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Pred. No. 5e-90;
.3; Mismatches 163;
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PREDE

18-MAR-1998 W29258 standard; W29258;

(first entry)

receptor

associated

factor

family protein.

receptor;

Protein;

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Human TRAF5, a novel TNF recep TRAF5; tumour necrosis factor TNF signal transducer system.

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Best Local Similarity
Matches 243; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferation inhibitor
Claim 2; Pages 41-44; 80pp; Japanese.
The present sequence is murine TRAF5 a protein of the tumour necrosis factor (TNF) receptor associated factor family. TRAF5 products can be used in immunisation, to treat allergies and as cell proliferation inhibitors. They can also be used to screen TRAF5 inhibitors or regulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAF5, protein of tumour necrosis factor receptor associated family - useful in immunisation, to treat allergies and as co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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11-APR-1996;
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                                                                                                                  HSEEQAAVPCAFIRQNSGNSISLDFEPDTEYQFVEQLEERYKCAFCHSVLHNPHQTGCGH
            TVLEN--GTYIKDDTIFIKVIVDTSDLPD
                                                                                                                                                                                                           VTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIW 419
                                                                                                                                                                                                                                                            EMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQ--NWE----EADSMKSSVESLQNR 359
                                                                                                                                                                                                                                                                                                                                       QIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFCQQCIRSLRELNSVPICPVDKEVIKPQEVFKDNCCKREVLNLHVYCKN-APGCNARII 121
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 STLENSKNTYIKDDTLFLKVAVDLTDLED
                                                            EFDSLLQWPFRQRVTLMLLDQSGKKNHIVETFKADPNSSSFKRPDGEMNIASGCPRFVSH 528
                                                                         EYDALLPWPFKQKYTLMLMDQGSSRRHLGDAFKPDPNSSSFKKFTGEMNIASGCPVFVAQ 539
                                                                                                                                                                                                                                                                                                         NLLEHERAALQDHMLLVLEKNYQLEQRISDLYQSLEQKESKIQQLAETVKKFEKELKQFT
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                                                                                                                                                                                                                                                                                                                                                                                                  IALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQ 245
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                                                                                                                                                                                                                                           QMFGRNGTFLSNVQ-ALTSHTDKSAWLEAQVRQLLQIVNQQPSRLDLRSLVDAVDSVKQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                              QRLVLLEGETSKHDAHINIHKAQLNKNEERFKQLEGACYSGKLIW
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42.78;
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Pred. No. 5e-
15; Mismatches
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557
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5e-90;
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12;

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PP 24-FEB-1997; J00512.

PR 24-FEB-1996; JP-034674.

PR (SUME) SUMMINON ELECTRIC IND CO.

PA (SUME) SUMMINON ELECTRIC IND CO.

PA Nakano H, Nakata M, Okumura K, Yagita H;

PI Nakano H, Nakata M, Okumura K, Yagita H;

PI NAFS - useful to study signal transduction in tumour necrosis

PT TRAFS - useful to study signal transduction in tumour necrosis

PT TRAFS - useful to study signal transduction in tumour necrosis

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CC claim 3; Pages 46-49; 69pp; Japanese.

CC factor family. The TRAFS protein has a coiled-coll domain, a leucine

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CC collos or TRAF protein has a coiled-coll domain, a leucine

CC collos or TRAF receptor 2. TRAFS and its corresponding DNA are useful for

CC the investigation of the signal transducer system of the TNF receptor

CC family and the functions of TRAF proteins. They can also be used as

CC probes for research and diagnostic purposes, and investigation of the

Specific applications of potential therapeutic agents.
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